GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compuç

Compugen Ltd.

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Minimum DB
Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 15, 2003, 02:58:27; Search time 256 Seconds (without alignments) 9299.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*
1: /cgn2 6/ptodata/1/~~~
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11:
12:
13:
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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:/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	1756	513509	7766	7766	941	1784	1589	861	1599	1584	1527	, 1757	1599	1620	2397	1584	647	1801	1644	Query Match Length
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The state of the s	7	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 464, App	Sequence 15, Appl	Æ	Sequence 187, App	Sequence 1762, Ap	Sequence 1765, Ap	Sequence 72, Appl	Sequence 70, Appl	Sequence 281, App	Sequence 2266, Ap	Sequence 3, Appli	Sequence 1942, Ap	Sequence 554, App	Sequence 30, Appl	Sequence 1, Appli	Description

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US-09-938-842A-2575	US-09-258-031B-74	US-09-738-626-1	US-09-738-626-1095	US-10-123-155-512	US-09-764-868-173	US-09-954-531-580	US-09-954-531-158	US-10-071-751-41	US-09-938-842A-222	US-10-047-412A-3	US-09-738-626-1	US-09-738-626-2031	US-09-864-761-8758	US-09-938-842A-319	US-09-258-031B-57	US-10-239-676-203	US-09-258-031B-24	US-09-878-574-18	US-09-258-031B-43	US-09-258-031B-42	US-10-329-960-1	US-09-258-031B-45	US-09-770-149-927	US-09-924-035A-19	05-10-114-043-1
Sequence 2575, Ap	Sequence 74, Appl	Sequence 1, Appli	Sequence 1095, Ap	Sequence 512, App			Sequence 158, App	Sequence 41, Appl	Sequence 222, App	Sequence 3, Appli	Sequence 1, Appli	Sequence 2031, Ap	Sequence 8758, Ap	Sequence 319, App	Sequence 57, Appl	Sequence 203, App	Sequence 24, Appl		Sequence 43, Appl		Sequence 1, Appli	Sequence 45, Appl	Sequence 927, App	Sequence 19, Appl	sequence I, Appril

## ALIGNMENTS

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; Sequence 1, Application US/09998284
; Patent No. US20020106361A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: COMPOSTION
    FILE REFERENCE: 674509-2035
; CURRENT APPLICATION NUMBER: US/09/98,284
; CURRENT ETILING DATE: 2001-11-30
    PRIOR APPLICATION NUMBER: US/09/98,284
; PRIOR APPLICATION NUMBER: GB 9913050.2
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US-09-998-284-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1644
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 1644; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Chondrus crispus
                                                                              121
                                                                                                   121 GGTACCAACATCGATTTCGTTTTACGTCGTTTACACTCCACAAGGTGCTTGTACTGCTTTG 180
                               181 GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT 240
181
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  GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT
                                                                                                                                                            CCAGACAAGCCTGACCCAAGATTGCCATCCATGAAGCAAGGTTTCAACAGAAGATGGATT
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100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                               Length 1644;
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0; Gaps

240

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	1321 CAGGAAGAAGACAAGGATGCAGTTAACTTGAAGTGGATTAGAGACTTTTACGAGGAGATG 1380
	1261 GATGCTACTGCAGTTGCTCAGAGAGAGATACATCATCAAACTGCAGTACCAGACATACTGG 1320
·	1201 ATGAAGGATGCTCTTCTCAGGTTGATATGTTCGGTGGTGAGATTCACAAGGTTGTTTGG 1260
	1141 CAGATTGATGTTATCTGGAAATACCTTACTGAGGTTCCTGACGGTTTGACTAGTGCCGAA 1200
	1081 GGTCCTAATCAGAGAGGGTAAGTACAAGTCTGCTTACATGATCAAGGACTTTCCAGACTTC 1140
	1021 ATGCATGACGAGACTATGGACTACCCTTTCTACGCTTTGACTGAGACTATCAACGGTTCC 1080
	961 GCTGGTTGGGCTCCTTTCCCTGTTAGACCTAGAAAGAGACACACATCCAAGACTTCTTAT 1020
	901 GAGGCTGACATTGAACAGATCTACAAAACATGCGAGCCTACCAAAGCTCTTGGTGGTCAT 960 
	841 TATACATCCTACTCTAACGACGCCGAGAGAGAGAGATTGCCCAAGACAGAC
···-	781 AATACTGTTGGTAAGTTCCAAATCTTCCACCAAGCAGCTGAAGAGTTTGTTATGTACTTG 840
	721 AGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTCAAGTTGGCTAGATGTGATTGGAAG 780 
	661 CCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACACTTCTCTTTGGGACGGTTTCACT 720
	601 CACACTGGTGGAGGTGGAGGTAACTTCGGTATTATCACCAAATACTACTTCAAGGATTTG 660
	541 TCTGTTCTTAAGTACGTTCACAAGGATTCCGAAGGTAACGACGGTGAGTTGTTTTTGGGCT 600
	481 TTGCCAGTCGATTGGTTATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGAC 540
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	361 TCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTGCCAGGTGGTTCCTGTTACTCC 420
	301 GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTTCCGGTGACACCAACTGGGGT 360 
	241 TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTGGTT 300

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RESULT 2
US-09-824-053-30
; Sequence 30, Application US/09824053
; Patent No. US20020106725A1
; GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 30: US-09-824-053-30
                                                                                           REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEPAX: (202) 778-2201
TELEFAX: (202) 778-2201
TELEX: NO. US20020106725A1e
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1801 base pairs
TYPE: nucleic acid
STRANDENMSS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,053
FILING DATE: 03-Apr-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION NUMBER: 08/669,304
FILING DATE: <UNknown>
APPLICATION NUMBER: 08/669,304
FILING DATE: <UNknown>
APPLICATION NUMBER: 08/669,304
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Peter Stougaard
Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1621
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                                                                                   FEATURE:
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                                        NAME/KEY: CDS
LOCATION: 84..
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Query Match Best Local S Matches 1416	#Atch 77.8%; Score 1279.2; DB 10; Length 1801; cal Similarity 86.1%; Pred. No. 0; s 1416; Conservative 0; Mismatches 228; Indels 0; Gaps 0;	
B X	1 ATGGCTACTTTGCCACAAAAGGACCCAGGTTACATTGTTATTGACGTCAACGCTGGTACT 60	
8 8	61 CCAGACAAGCCTGACCAAGATTGCCATCCATGAAGCAAGGTTTCAACAGAAGATGGATT 120	
8 8	121 GGTACCAACATCGATTTCGTTTACGTCGTTTACACTCCACAAGGTGCTTGTACTGCTTTG 180	
B 5	181 GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT 240	
96 A2	241 TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTTGGTT 300	
96 29	301 GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTCTC	
8 8	361 TCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTTGCCAGGTGGTTCCTGTTACTCC 420	
₩ ₩	421 GTCGGTTTGGGTGGTCACATTGTCGGTGGAGGTGACGGTATTTTTGGCCAGATTGCACGGT 480	
95 PA	481 TTGCCAGTCGATTGGTTATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGAC 540	
B 53	541 TCTGTTCTTAAGTACGATCACAAGGATTCCGAAGGTAACGACGGTGAGTTGTTTTGGGCT 600	
용 왕	601 CACACTGGTGGAGGTGAAGTTACTTCGGTATTATCACCAAATACTACTTCAAGGATTTG 660	
B &	661 CCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACACTTCTCTTGGGACGGTTTCACT 720	
D QY	721 AGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTCAAGTTGGCTAGATGTGGAAG 780	
D Q	781 AATACTGTTGGTAAGTTCCAAATCTTCCACCAAGCAGCTGAAGAGTTTGTTATGTACTTG 840	
Qy Db	841 TATACATCCTACTCTAACGACGCCGAGAGAGAGAGTTGCCCAAGACAGAC	
9d V2	901 GAGGCTGACATTGAACAGATCTACAAAACATGCGAGCCTACCAAAGCTCTTGGTGGTCAT 960 	
B &	961 GCTGGTTGGGCTCCTTTCCCTGTTAGACCTAGAAAGAGACACACATCCAAGACTTCTTAT 1020	

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TTTGAGGGATGCTACCTTCAACTACCCTGATGTTGACCTGGAACACTGGAAGAACGGTAAG
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                                                                                                                                                                                                                                                                            TTGTGGGATCCTAACGAGATCTTCACAAACAAACAGTCTATCCCTACTAAACCTCTTAAG
                                                                                                                                TATGAGCCTTATGGTGGTGTTCCAGACCCTAACACTCAGGTTGAGAGTGGTAAAGGTGTT
                                                                                                                        TATGAGCCGTATGGCGGGTTCCAGACCCCAACACGCAGGTGGAGAGTGGTAAAGGTGTG
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RESULT 3

US-09-770-149-554/c

J Sequence 554, Application US/09770149

Patent No. US20020059663A1

GENERAL INFORMATION:

APPLICANT: Hamilton, Carol M.

APPLICANT: Hamilton, Carol M.

APPLICANT: Hamilton, Carol M.

APPLICANT: Paice, Jennifer L.

APPLICANT: Yu, Yang

APPLICANT: Rameaka, Joshua G.

APPLICANT: Page, Amy

APPLICANT: Hatchew, Abraham V.

APPLICANT: Ledford, Brooke L.

APPLICANT: Woessner, Jeffrey P.

APPLICANT: Haas, William David

APPLICANT: Garcia, Carlos A.

APPLICANT: Kricker, Maja

APPLICANT: Slader, Ted

APPLICANT: Allen, Keith R.

APPLICANT: Hurban, Patrick

TITLE OF INVENTION: Expressed Sequences of

TITLE OF INVENTION: Expressed Sequences of

TITLE OF INVENTION: Harban, Carlos A.

FILE REFERENCE: 2024 (PARA-013PRV)

CURRENT APPLICATION NUMBER: US/09/770,149

Arabidopsis

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PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FASTSEQ for Windows Version 4
SEQ ID NO 554
LENGTH: 647
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1942
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Best Local Similarity 50.2%;
Matches 103; Conservative
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SEQ ID NO 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1942, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE PILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
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APPLICANT: Wang
APPLICANT: Zhu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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FRATURE:

FRATURE:

LOCATION: (1)...(647)

OTHER INFORMATION: n = A,T,C or
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                                                                                                        435 TCACATTGTCGGTGGAGGTGACGGTATTTTGGCCAGATTGCACGGTTTGCCAGTCGATTG 494
                                                                                                                                                                                                                                       417 CGAGAGAACGGCTTGGGTTGATTCTGGTGCTACCCTCGGAGAGCTTTACTATAGAATCTC 476
                                                                                                                                                                                                                                                                                  315 CGACGATAGAGGTTACTTCGTCTCTCCGGTGACACCAACTGGGGTTCCTTCAAGACCTT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 TTCTTCAAGAACGAGCAGAGTATTCCTCCGGTTCGTGTAAAGTAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 TATTTCTTGGGGAATTTGAAGAGATTGATGGTTAAAGCTAAGTATGATCCTGATAAT 194
GTTATCCGGTGTTGAAGTTGTCGTT 519
                                                                                                                                                     TGAGAAGAGCAATGTTCTTGGATTTCCGGCGGGTTTGTCTACCACATTGGGCGTTGGTGG
                                                                                                                                                                                FastSEQ for Windows Version 4.0
                                                                  ACACTTTAGCGGCGGAGGATACGGTAATCTGATGAGAAAGTATGGTTTGTCGGTGGATAA
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Pred. No. 0.0047;
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US-10-170-656-3
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                                                                   US-09-938-842A-2266
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APPLICANT: Lindquist, Susan K.
APPLICANT: Queltsch, Christin
APPLICANT: Sangster, Todd A.
                                                                                                                             NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2266
LENGTH: 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2266, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Sangster, Todd A.
TITLE OF INVENTION: Methods and Compositions for Revealing Hidden Generic Variation
FILE REFERENCE: ARCD:377US1
FULL REFERENCE: ARCD:377US1
CURRENT APPLICATION NUMBER: US/10/170,656
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/298,211
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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PRIOR APPLICATION NUMBER: US 60/379,484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
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2.5%;
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Score
Pred.
41.4; DB
No. 0.022;
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                    Length 1620;
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Best Local Similarity

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APPLICANT: Kreps, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Edu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 281
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US-09-258-031B-70
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                                                                                                                                                          Sequence 70, Application US/09258031B Patent No. US20020168735A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1599
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                      APPLICANT:
                                                       APPLICANT:
                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                         636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
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                                                                                                                                                                                                                                                                                         TGTCG 640
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                                                                                                                                                                                                                                                                                                                             IGICG
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PONSTEIN, Anne S
LAGEWEG, Wessel
PONSTEIN, Anne S
                                                                   MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna Pieternella
                                                                                                  STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BRIAGE, Marianne Beatrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                       LAGEWEG, Wessel
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   Anne Silene
                                   Anne Silene
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Pred. No. 0.055;
0; Mismatches 53;
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                GENERAL INFORMATION:
APPLICANT: STUTUES
APPLICANT: CUSTERS
APPLICANT: SELA-BU
APPLICANT: MELCHER
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RESULT 9
US-09-258-031B-72
; Sequence 72, Appl
; Patent No. US2003
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSITION TO THE PRIOR APPLICATION NUMBER: PCT/EP97/04923
APPLICATION NUMBER: PCT/EP97/04923
FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP97200831.2
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pair
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy disk
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ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: FEATURE:
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ORGANISM: Aral
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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ZIP: 10023 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                  513
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                                                                                                                                                                                                                                    438 AGCTTATCCCGCCGGAATTTGTCCCACGGTTGGTGTCGGTGGCCATATCAGTGGTGGAGG
                                                                                                                                                                                                                                                         393 AGTTTTGCCAGGTGGTTCCTGTTACTCCGTCGGTTTGGGTGGTCACATTGTCGGTGGAGG
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                                                                                                                                                                    TTACGGTAACATGATGAGAAAATACGGTCTCACCGTAGATAATACCATCGATGCAAGAAT
               Application US/09258031B
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Pred. No. 0.13;
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Gaps

512 497 452 0

STUIVER, Maarten Hendrik CUSTERS, Jerome Humbertina Henricus Victor SELA-BUKLAGE, Marianne Beatrix MELCHERS, Leo Sjoerd VAN DEVENTER-TROOST, Johanna Pieternella

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US-09-938-842A-1765

Sequence 1765, Application US/09938842A

; Patent NO. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/04923
PILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP97200831.2
PILING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP96202466.7
PRIOR APPLICATION NUMBER: EP96202466.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-SEP-1996
INFORMATION FOR SEQ ID NO: "SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1527 base pairs
TYPE: nucleic acid
CTENAUSEDNESS: Acuble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NC ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Arab
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ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.25" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
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TITLE OF INVENTION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
STRAIN: Colombia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-FEB-1999
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LOCATION: 1...
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                                                                                                                                                                           513
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PONSTEIN, Anne Silene
LAGEWEG, Wessel
PONSTEIN, Anne Silene
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56.8%;
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Pred. No. 0.18;
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1762
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1765
LENGTH: 1584
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                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1762
LENGTH: 1599
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                                                                                    Matches
                                                                                                      Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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                                      297 GGTTGAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTTCCGGTGACACCCAACTG 356
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420 GGTTGACGTTGATTTGGACAGTAACAGTGCGTGGGCTCATGCTGGTGCTACCATCGGAGA 479
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Wang, Xun
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                                                                                                        Score 37.2; DB Pred. No. 0.54;
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Pred. No. 0.18;
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                                                                                    93;
                                                                                                                           Length 1599;
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                                                                                    Gaps
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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-187
                                                                                                                 RESULT 13
US-09-258-031B-19
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US-09-801-368-187/c
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                                                                 Sequence 19, Application US/09258031B Patent No. US20020168735A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-01-19
PRIOR PILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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APPLICANT:
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Cali, Brian
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                                                                                                                                                                                     TGTTGCTGCTGTTG 535
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Sherman, Amir
Silva, Jeff
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Maxon, Mary
Milne, Todd
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Holtzman, Doug
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              STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BURLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
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54.5%;
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Best Local S
Matches 70
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1589 base pair:
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PRIOR APPLICATION DATA:
APPLICATION UNMERS: PCT/EP97/04923
FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION UNMERS: EP97200831.2
FILING DATE: 19-MAR-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy dis
COMPUTER: IBM PC compatible
COMPUTER: WINDOWS 95
COFFWANDS. WORDBEREFOR
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     FEATURE:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
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CURRENT APPLICATION DATA:
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LOCATION:
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COUNTRY:
                                                                                                                                                                                                                                                                                                  STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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616 ATAGAT 621
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                                                                                                                                                394 GTTTTGCCAGGTGGTTCCTGTTACTCCGTCGGTTTGGGTGGCTCACATTGTCGGTGGAGGT 453
                                                                                                                                                                                             Similarity
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                          GTCGTT 519
                                                          TÄTGGTÄATTTGATGÄGAAAATÄTGGTTTGTCGGTTGATAATATTGTTGATGCTCAAATA 615
                                                                                      GACGGTATTTTGGCCAGATTGCACGGTTTGCCAGTCGATTGGTTATCCGGTGTTGAAGTT 513
                                                                                                                    GGTTTTCCGGCAGGGGTTTGTCCAACGGTTGGCGTTGGTGGGCATTTTTAGTGGTGGTGGG 555
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26 WEST 61 STREET
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VENTION: ANTIFUNGAL PI
                                                                                                                                                                               Conservative
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RESULT 14 US-09-258-031B-15 ; Sequence 15, Application US/09258031B ; Patent No. US20020168735A1 ; GENERAL INFORMATION:

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; LOCATION:
US-09-258-031B-15
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Best Local Similarity 55.6%;
Matches 70; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/EP97/04923
FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helia
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS 95 SOFTWARE: WORDPERFECT 8 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/258,031B
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MEDIUM TYPE: 3.25" Floppy disk
                                                                                                                                                                                                                                                                                                                                  FEATURE:
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ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
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ZIP: 10023 - 7604
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636
                                  514 GTCGTT 519
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double
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PONSTEIN, Ann.
PONSTEIN, Messel
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PONSTEIN, Anne Silene
VENTION: ANTIFUNGAL PROTEINS, DNA CODING
VENTION: THEREFOR, AND HOSTS INCORPORATING
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                                                                                                                                                                                                                         Score 36.4; D
Pred. No. 1.1;
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                                                                                                                                                                                                         56; Indels
                                                                                                                                                                                                                                          Length 1784;
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RESULT 15

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; ORGANISM: Homo Sapien
US-10-123-155-464
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30 CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15
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831 EFPQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQFSTRTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AAGATTGCCATCCATGAAGCAAGGTTTCAACAGAAGATGGATTGGTACCAACATCGATTT 137
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                                    ATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGACTCTGTTCTTAAGTA 554
                                                                              VFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALCRTQNKEKLQWLLDESFKGDKIKTQ
                                                                                                                     CATTGTCGGTGGAGGTGACGGTATTTTGGCCAGATTGCCACGGTTTGCCAGTCGATTGGTT 497
                                                                                                                                                             IDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKESNGNLSLPVDVTLA
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Filvaroff, Ellen
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Search completed: June 15, 2003, 06:21:33 Job time : 260 secs

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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US-08-403-379A-5
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US-08-921-93-14
US-08-480-921B-3
US-08-481-921-17
US-08-08-746-111-4
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PCT-US-93-00869-17
US-08-971-918-917
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sequence 3, Appli
sequence 17, Appli
sequence 1, Appli
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sequence 5, Appli
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sequence 92, Appl
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31.2	31.2	31.2	31.2	31.2	31.4	31.4	31.4	31.4	31.4	31.4	31.8	31.8	31.8	31.8	31.8	31.8	31.8
1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
2424	2424	2424	2424	915	4411529	4403765	7577	6854	1546	703	4411529	4403765	6156	6156	1344	1303	1303
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US-09-398-395A-45	US-09-865-171-1	US-09-360-545-15	US-09-234-393-1	PCT-US94-01149-56	US-09-103-840A-1	US-09-103-840A-2	US-08-961-527-46	US-08-961-527-200	US-08-961-083-21	US-08-858-207A-21	US-09-103-840A-1	US-09-103-840A-2	US-09-723-535-3	US-08-891-640-1	US-08-902-585-1	US-09-126-192A-1	US-08-844-154-1
4.5	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 56, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 46, Appl	Sequence 200, App	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

## ALIGNMENTS

RESULT 1 US-08-669-304-30

Sequence 30, Application US/08669304 Patent No. 6251626

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US-08-669-304-30
                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20006-1109
ZIP: 20006-1109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION + 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.00003
TELEPHONE: (202) 955-1926
TELEPHONE: (202) 778-2201
TELEPHONE: (202) 778-2201
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APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                 TELEX: NO. 6251626e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                        TOPOLOGY: 1i
MOLECULE TYPE:
                                                                  FEATURE:
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                     NAME/KEY:
LOCATION:
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CITY: Washington
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                linear
                                                                                        DNA (genomic)
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Query Match

77.8%; Score 1279.2;

DB 4;

Length 1801;

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Best Local Similarity Matches 1416; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTCCGGTGACACCCAACTGGGGT
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                  ATGCATGACGAGACTATGGACTACCCTTTCTACGCTTTGACTGAGACTATCAACGGTTCC
                                                      GCTGGGTGGGCCGTTCCCCGTGCGGCCGCGCAAGAGGCACACATCCAAGACGTCGTAT
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Conservative
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                                                                                                                                                                                                    Sequence 1, Application US/09036987A
Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Broughton, Mary C.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Gen
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-036-987A-1/c
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            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                       ZIP: 46268
COMPUTER READABLE FORM:
                                                                                                                                                        STREET: 9330 Zionsville
CITY: Indianapolis
STATE: Indiana
   APPLICATION NUMBER:
                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1704
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 US/09/036,987A
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                                      Version
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FILING DATE:

09-MAR-1998

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GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
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REPERENCE/DOCKET NUMBER: 50,60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEPAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH OF SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09370700 Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.6%;
Best Local Similarity 52.3%;
                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 157;
                                                                                              TYPE: DNA
ORGANISM: Saccharopolyspora spinosa
-09-370-700-1
                                                                                                                                                           LENGTH: 80161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15796 GTCACGACTTGTGGTGGGCGCACACCGGTGGCGGTGGCGGCAACTTCGGGATCGTCACCA 1573:
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          Conservative
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                              3.6%; Score 60; DB 4; 52.3%; Pred. No. 4.5e-08;
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Pred. No. 4.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 140;
             Mismatches
                                                    DB 4; Length 80161;
               140;
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SOFTWARE: Patentin V
SEQ ID NO 15
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-09-29
RIOR APPLICATION NUMBER: EP 98201024.1
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: ECT/EP99/02178
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stuiver, Maarten
APPLICANT: Custers, Jerome
APPLICANT: Simons, Lambertus
TITLE OF INVENTION: Pathogen-Inducible Promoter
FILE REFERENCE: MOG 57707/UST
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                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(1889)
NAME/KEY: CDS
LOCATION: (1890)..(3503)
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helianthus annuus
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ATAGAT 2537
                                                                                                            GACGGTATTTTGGCCAGATTGCACGGTTTGCCAGTCGATTGGTTATCCGGTGTTGAAGTT 513
                                                                                                                                                 GGTTTTCCGGCAGGGGTTTGTCCAACGGTTGGCGTTGGTGGGCATTTTAGTGGTGGTGG
                                                                                                                                                                                   GTTTTGCCAGGTGGTTACTCCGTCGGTTTGGGTGGTCACATTGTCGGTGGAGGT 453
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                                                                                                                                                                                                                        Conservative
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55.6%;
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                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                         Length 3680;
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US-09-125-619-3
; Sequence 3, Application US/09125619
; Patent No. 6437116
; GENERAL INFORMATION:

APPLICANT:

NORRIS,

STEVEN J.

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LENGTH: 7766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Pararry
           APPLICATION NUMBER: US/08/155,906
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/850,909
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
LOCATION: (127)
OTHER INFORMATION: R = A OR
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ORGANISM: Borrelia burgdorferi
FEATURE:
                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ICHIHARA, SHIGH APPLICANT: MIZUNO, TAKESHI
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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 No. 5405777man F.
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Pred. No. 0.78;
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Matches
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SOFTWARE: Patentin Ver.
SEQ ID NO 17
SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                LOCATION: (379)
OTHER INFORMATION: replace (379, ", NAME/KEY: unsure
LOCATION: (786)
OTHER INFORMATION: replace (786, ", NAME/KEY: unsure
LOCATION: (1105)...(1106)
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/647,390
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: EP 98201024.1
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: PCT/EP99/02178
PRIOR FILING DATE: 1999-03-25
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Custers, Jerome APPLICANT: Simons, Lambertus APPLICANT: Simons, Lambertus APPLICANT: OF INVENTION: Pathogen
OTHER INFORMATION: replace (1105..1106, "ga"
                                                                                                                                                       LOCATION: (372)
OTHER INFORMATION: replace (372,
NAME/KEY: unsure
                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (7)..(1626)
                                                                                                                                                                                                                                                                                                   ORGANISM: Lactuca sativa
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                         NAME/KEY: unsure
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                        LENGTH: 1981
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TOPOLOGY: linear
MOLECULE TYPE: DNA
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LENGTH: 1632 base pair
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les 86; Conserv
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STRANDEDNESS: double
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Pred. No. 0.51;
0; Mismatches 8
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"gg" or "aa")
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Best Local Similarity

2.1%;

Score 33.8; DB Pred. No. 1.4;

4.

Length 1981;

Query Match

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Patent No. 5304371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
TITLE OF INVENTION: Peptide for Diagnosing and Immunizing
TITLE OF INVENTION: Against T. cruzi Infection
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Trypanosoma cruzi
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                               ACLECCE: NO
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                                                                                              Local Similarity 51.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-FEE CLASSIFICATION: 53
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REFERENCE/DOCKET NUMBER: REED
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                                                                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                   LOCATION:
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268 GTCAAGGCTATTATCAACGTTACTGGTTTGGTTGAATCTGGTTACGACGACGATAGAGGT 327
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                                                               208 GGTACCGTCAGAATCGTTTCTGGTGGTCACTGTTACGAAGACTTCGTTTTCGACGAATGT 267
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                               GGCTCCGCTGATTTCGGCTCCGCTGGTTTTGGCTCCGCTGACTTCGGCTCCGCTGGTTTA 496
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                                                                                              Score 33.4; DB Pred. No. 0.93; 0; Mismatches
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US-08-169-563-1
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US-08-169-563-1/c
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                                                                                                                         Matches
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                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Tryp.
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-DEC-1995
FILING BATE: 17-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/836,642
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Op
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                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,69 REFERENCE/DOCKET NUMBER: 1
                                                                                                                         Local Similarity 51.0
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                                                                                                                                                                                                                                                      CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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GGCCCCGCTGATTTCGACTCCGCTGGTTTGGGCTCTGCTGATTTCGGCTCCGCTGGTTTG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,693
ER: REED-A
                                                                                                                         0;
                                                                                                                        Score 33.4; DB Pred. No. 0.93; 0; Mismatches
                                                                                                                                                    DB 1;
                                                                                                                         76;
                                                                                                                                                     Length 636;
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328 TACTICGICTCTTCCGGTGACACCAACTGGGGTTC 362

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PATENT NO. 5756662
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: OF T. CRUZI INFECTION
                                                                          Sequence 5, Application US/08929414 Patent No. 5942403
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MAKK, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
       APPLICANT:
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LOCATION:
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ZIP: 98104-7092
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                                                                                                                                                                                                                            328 TACTTCGTCTTCCGGTGACACCAACTGGGGTTC 362
                                                                                                                                                                                                                                                                                                                                         555 GGCTCCGCTGATTTCGGCTCCGCTGGTTTTGGCTCCGCTGACTTCGGCTCCGCTGGTTTA 496
                                                                                                                                                                                                                                                                                                                                                                           208 GGTACCGTCAGAATCGTTTCTGGTGGTCACTGTTACGAAGACTTCGTTTTCGACGAATGT 267
                                                                                                                                                                                                                                                                                                    268 GTCAAGGCTATTATCAACGTTACTGGTTTGGTTGAATCTGGTTACGACGACGATAGAGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                 79;
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                                                                                                                                                                                                                                                                  GGCCCCGCTGATTTCGACTCCGCTGGTTTGGGCTCTGCTGATTTCGGCTCCGCTGGTTTG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 682-6031
(206) 682-6031
Reed, Steven G.
Haughton, Raymond
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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US-09-217-490-1
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09217490 Patent No. 6165761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                             APPLICANT: Schneider, Palle
APPLICANT: Christensen, Soren
APPLICANT: Dybdal, Lone
APPLICANT: Fuglsang, Claus Crone
APPLICANT: Xu, Feng
APPLICANT: Xu, Feng
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: Carbohydrate Oxidase And use
TITLE OF INVENTION: Baking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,414
FILING DATE: 15-SEP-1997
CLASSIFICATION: 530
                FILE REFERENCE: 5421.200-ÜS
CUURENT APPLICATION NUMBER: US/09/217,490
CURRENT FILING DATE: 1998-12-21
EARLIER APPLICATION NUMBER: PA 1997 01505
EARLIER FILING DATE: 1997-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
MARLIER APPLICATION NUMBER: PA 1998 00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 TACTTCGTCTCTTCCGGTGACACCAACTGGGGTTC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555 GGCTCCGCTGATTTCGGCTCCGCTGGTTTTGGCTCCGCTGACTTCGGCTCCGCTGGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 GGTACCGTCAGAATCGTTTCTGGTGGTCACTGTTACGAAGACTTCGTTTTCGACGAATGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
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; EARLIER FILING DATE: 1998-06-04;
; EARLIER APPLICATION NUMBER: 60/068,717;
; EARLIER FILING DATE: 1997-12-23;
; EARLIER APPLICATION NUMBER: 60/088/725;
EARLIER FILING DATE: 1998-06-10;
NUMBER OF SEQ ID NOS: 23;
; SOFTMARB: FBStSEQ for Windows Version 3.0;
SEQ ID NO 1;
LENGTH: 1553
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                                                Query Match
Best Local Similarity
Matches 83; Conserve
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                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 3
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                                                                                                                                                                                                                                                                                        APPLICANT: Potter, Sharon L.
APPLICANT: Wegrich Lynette M.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30780A
CURRENT APPLICATION NUMBER: US/09/480,921B
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Levin, Joshua Z.
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LOCATION:
                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)..(1458)
                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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LOCATION: (1012)..(1076)
                                                                                                                                                                                        FEATURE:
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LOCATION: (67)..(1550)
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ORGANISM: Microdochium nivale
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                                                                                                                                                                                                                                           ENGTH: 1458
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Local Similarity 49.2%;
les 88; Conservative
                         1342 GTTAACTTGAAGTGGATTAGAGACTTTTACGAGGAGATGTATGAGCCTTATGGTGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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28
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(1)..(1011)
GCTGATTTGGACGAGTTATCTGACAATGAAGCAGAATTGGACGAGAATGATGGTGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACGGTACATGCCCTGGTGTCGGCATCTCCGGCCACTTTGCCCACGGCGGCTTCGGCT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGTGGTTCCTGTTACTCCGTCGGTTTGGGTGGTCACATTGTCGGTGGAGGTGACGGTA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                Budziszewski,
                                                                   Conservative
                                                                               50.0%;
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                                                                   0
                                                                 Score 33.2; DB Pred. No. 1.8; 0; Mismatches
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Pred. No. 1.7;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harr
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Patent No. 5
                                                                                                                                                                         Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILLING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26.AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                    1423
                                                                                                       1483 GTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRR 1424
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1217 TTCAGGTTGATATGTTCGGTGGTGAGATTCACAAGGTTGTTTGGGATGCTACTGCAGTTG 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                         26;
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5670367
                                    GGAAATACCTTACTGAGGTTCCTGACGGTTTGACTAGTGCCGAAATGAAGGATGCTCTTC
                                                                                                                                       GTAAGTACAAGTCTGCTTACATGATCAAGGACTTTCCAGACTTCCAGATTGATGTTATCT 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCCTGATGTTGACTTGAACAACTGGAAGAACGGTAAGTATGGTG 1507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAAGGAAGAAGATGTTGATATGGATATGGCTGATTTAGAGACACTTAACTATGAT 147
                                                                                                                                                                                                                                                         pTZgpt-F1s
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                  7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FALKNER, F. G.
VENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                             single
                                                                                                                                   2.0%; SCULL
6.2%; Pred. No. 5.2;
6.10 Pred. No. 5.2;
9.11ve 203; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP 91 114 300.6
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                                                                                                                                                                                                        Length 7218;
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US-08-630-822A-92/c
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                                                                                                                                                                                                                          US-08-630-822A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 92, Application US/08630822A Patent No. 5840695
                                                                                                                                                Query Match 2.0%;
Best Local Similarity 53.5%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: FRANK,
                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLCCY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/630,82;
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HUNTER, S
APPLICANT: WALLENFEI
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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ZIP: 80203
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                                                                                                     208 GGTACCGTCAGAATCGTTTCTGGTGGTCACTGTTACGAAGACTTCGTTTTCGACGAATGT 267
                                 268 GTCAAGGCTATTATCAACGTTACTGGTTTGGTTTGAATCTGGTTACGACGACGACGATAGAGGT 327
                                                                        213 GGTATAGCCAGTGGTATCCAGTGGTGACTGGTGCGGAAACTACGTTGGTGGTGACGTA 154
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: Colorado
GTCATTGGCAAGATGTCCGGTGGTGTATCCAGTAACTGGAGTGGATACAACATTGGTGGT
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1700 Lincoln Street, Suite 3500
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HUNTER, SHITLEY WU
WALLENFELS, LYNDA
VENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
VENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                            (303) 863-9700
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2618-17-C3
                                                                                                                                              Score 33; DB 2; Length 490; Pred. No. 1.1; 0; Mismatches 60; Indels
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Search completed: June 15, 2003, 02:58:25 Job time: 82 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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Perfect score:
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1: em
2: em
3: em
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(without alignments)
10823.325 Million cell updates/sec
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10:
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Gapop 10.0 , Gapext 1.0
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1644
1 atggctactttgccacaaaa.....ctaagcagactaaatagtag 1644
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em_estov:*
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em_estf4:*
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em_esthum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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42.6	42.6	42.8 8	1 42.8	Score
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4	634	632	624	608	603	577	573	542	540	437	360	770	647	565	524	492	350	769	633	600	537	493	387	360	360	360	807	688	595	569	416	406	1101	409	748	442	440	400
10	10	17	13	17	13	14	13								13	9	13	10	14	12	13	13	12	14	13	10	17	14	14	14	12	10	17	14	14	10	10	10
41	AV938215		BM441131	8	BJ479961	BQ839404	71	BQ468825	AJ470389	BH611048	AJ470390	BH478648	AL509182	BF049993	BI594743	AI995621	BI594738	E4.3	BQ607036	F48	BM277996	3	BF428917	D76262	BI594749	AV440363	AQ957642	BQ990898	BU007777	BU013165	BF202701	AV805562	CNS00LO0	BQ060219	BQ841497	AV798159	AV798160	AV811765
AV941742 AV941742	AV938215 AV938215	ω	1 EBed(	RL-72	79961 BJ4799	WHE4165	BJ471443	BQ468825 HM02H09r	AJ470389 AJ470389	BH611048 SALK_0297	AJ470390 AJ470390	BH478648 BOHKR61TR	AL509182 AL509182	BF049993 As_tgz_20	BI594743 As_tgz_43	AI995621 701675986	BI594738 As_tgz_43	BE414425 SCU009.F0	BQ607036 BRY_2917	BF485368 WHE2310_G	BM277996 As_tgz_51	BM170559 EST573082	WHE1710_	D76262 CELK116B6F	As_tgz_		57642	QGF21G13	•	QGJ3015.	WHE1777		ñ	Ts1168	WHE4	59 AV	60 AV79816	65 AV81176

## ALIGNMENTS

RESULT 1

TIGR 9712 Medical Center Drive, R Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtownpetigr.org DNA is from a doubled haploi Seq primer: TR Seq primer: TR Class: sheared ends. Location/Qualifiers source 1646		BH695306/c LOCUS  DEFINITION  BOMLJ48TR  BOQ_2_3_KB Bra  RCCESSION  BH695306.  BH695306.  BH695306.1  GSS.  KEYWORDS  GSS.  BYABSICA Oleracea.  ORGANISM  Brassica oleracea
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtownbetigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Seq primer: TR Class: sheared ends.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcphyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  1 (bases 1 to 646)  1 (bases 1 to 646)  1 (bases 1, Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)  0ther GSSs: BOMLJ48TF Contact: Chris Town	BH695306  BOMLJ48TR BO_2_3_KB Brassica oleracea genomic clone BOMLJ48, DNA sequence. BH695306 BH695306 BH695306 GI:18767922 GSS. Brassica oleracea. Brassica oleracea

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BASE COUNT
ORIGIN
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AUTHORS
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            Query Match
Best Local Similarity
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 Matches
                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun 
Unpublished (2001)
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Town, C.D., Van Aken, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea
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                                                                                                                                                                                                                                                          Email: cdtown@tigr.org
DNA is from a doubled haploid
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04; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea.
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                                                                                                                                                                                                                                                                                                        Medical Center Drive, 301-838-3523
                                                                                                                                                                                                                                                                                            301-838-0208
   Conservative
                                                                                                                                                                                                                                sheared ends.
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/clone lib="BO 2 3 KB"
/clone Pib="FO 2 3 KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
a 162 c 220 g 141 t
                                                                        genomic DNA inserted into 191 c 151 g 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                      /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1:
                                                                                                                                                                   organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                   /db_xref="taxon:3712"
/clone="BOHZJ13"
                                                                                                                                                                                                               Location/Qualifiers
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Brassica oleracea genomic
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Score 42.8; DB 17;
Pred. No. 0.17;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                    sequencing
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Pred. No. 0.16;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                    Utterback, T. and Fraser, C.M. quencing of Brassica oleracea
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BstXI linkers"
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                               709;
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BOHZJ13, DNA
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BH432838
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGVZ24TR
                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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BOGVZ24TF BOGV Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled
Seq primer: TF
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   TGTTCGGTGGTGAGATTCACAAGGTTGTTTTGGGATGCTACTGCAGTTGCTCA----GAGAG 1285
                               TGGAGAAGCTTTGGGCGACAATGTTGAAAATTCAAGAACGTTGTGTGGATGCAGTGGAACC
                                                             CTGAGGTTCCTGACGGTTTGACTAGTGCCGAAATGAAGGATGCTCTTCTTCAGGTTGATA
                                                                                                                             CTGCTTACATGATCAAGGACTTTCCAGACTTCCAGATTGATGTTATCTGGAAATACCTTA
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                                                                                                                                                                                                                                              201
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         /clone_lib="BOGV"
/note="Vector: pHoS1; Site_1: BstXI; 2-3
genomic DNA inserted into pHoS1 using Bst
a 236 c 176 g 234 t
                                                                                                                                                                                                                                                                                                       /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGVZ24"
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                                                                                                       1579 ATCTTCACAAACAACAGTCTATCCCTACTAAACCTCTTAAGGAG 1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALK_063965 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_063965, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 420)
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                                                                                                                                                                                                                                                                                             directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 78 c 66 g 129 t
                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Ārabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Columbia 0"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 TATTTCTTGGGGAATTTGAAGAGATTGATGGATGTTAAAGCTAAGTATGATCCTGATAAT 193
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 640)
                                                                                                                                                                                                         AV784340 640 bp mRNA line AV784340 RAFL5 Arabidopsis thaliana cDNA clone mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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AV786257
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3-1-1 Koyadai, Tsukuba,
                                                                                                                 thale cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                             TTCTTCAAAAACGAACAGAGCATTCCTCCGGTTCGTGTAATGTAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTTTTTGGGTAACCTGAACAGATTGATCAAGGCCAAATGGTTGTGGGATCCTAACGAG 1578
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dehydration (1, 2, 5, 10, 24 hr) and cold (1,
hr) treatments"
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germination to mature seeds"
/lab_host="DH10B"
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/clone_lib="RAFL6"
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Pred. No. 0.
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, Ibaraki 305-0074,
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AUTHORS

Narusaka,M.,

Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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AV811765/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 TTCTTCAAAAACGAACAGAGCATTCCTCCGGTTCGTGTAATGTAG 107
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
                                                                                                                                                             Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
                                                                                                                                                                                                                                  Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
                                                                                                                                                                                                                                                                                 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa, T., Shib
and Shinozaki, K.
                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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142 c 106 g 202 t
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/clone="RAFL05-18-J21"
/clone_lib="RAFL5"
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/lab_host="SOLR"
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Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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Pred. No. 0.18
0; Mismatches
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                                                                                                                     Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length CDNA library was constructed essentially
An Arabidopsis full-length CDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FIC-I vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al., submitted for publication) digested with BamHI and SalI. clone is in a modified pBluescript vector. Please visit our we site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for fu
                                                                                                                                                                                                                                                                3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                      Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
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AV798160 RAFL9
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AV798160.1
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                                                                                                                                                                                                                                                                                                                                                                       Contact: Motoaki Seki
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/clone="RAFL09-15-D04"
                     /organism="Arabidopsis
/db_xref="taxon:3702"
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/lab_host="DH10B"
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/db_xref="taxon:3702"
/clone="RAFL09-69-I23"
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/dev\_stage="plants at various developmental stages

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AV798159/c
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                                                                                                                                                                                                                                                                                                                              Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Functional Genomics Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Motoaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
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/lab_host="DHIOB"
/note="Site_1: BamHI; Site_2: SalI; subjected dehydration (1, 2, 5, 10, 24 hr) and cold (1, hr) treatments"
                                                                                      /note="Site_1: BamHI; Site_2: SalI; subjected dehydration (1, 2, 5, 10, 24 hr) and cold (1, hr) treatments" 98 c 68 g 147 t
                                                                                                                                                         /lab_host="DH10B"
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/db xref="taxon:3702"
/clone="WAFL09-15-003"
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library_Aegilops s
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West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: oandersn@pw.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Olin Anderson
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                                                                                                                                              216
                                            Conservative
                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoXI; Site 2: XhoI, Plants were grown in a growth chamber at the University of California, Davis (Akhunov in Devorak's lab). Pre-metotic anthers were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made and the cDNA clones were in vivo excised to give pBluescript phagemids at the University of California, Davis (Akhunov in Devorak's lab). Plasmid DNA preparations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              speltoides
                                                                                                                                                                                  and DNA sequencing were performed
                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Pre-meiotic anthers"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="WHE4211_F11_L20"
/clone_lib="Aegilops spe
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                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="Anther"
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/cultivar="F2 from 2-12-4-8-1-1-(1)
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CNS00LO0 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                           87;
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409 bp mRNA linear EST 01-APR-2002
Ts1168 Thellungiella salsuginea ZAP cDNA library Thellungiella
salsuginea cDNA similar to reticuline oxidase - like protein, mRNA
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Wang Z.L., Li, P.H., Sun, Y.F., Zhang, Q., Zhao, Y.X. and Zhang, H.
Express.
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                                                                                                                                                                                                  GACGGTCGGTGTCGGAGGTCATTTAAGCGGCGGTGGGTACGGTAATATGCTGAGGAAGTT
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                                                                                                                              CGGATTGTCTGTCGATAACTTGATCGATGCGAAGATCGTCGAT 367
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Biology Department of Shandong Normal University
88, Wenhua East Road, Jinan, Shandong Province, 2
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(86)531-2966954
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                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: aerial part tissue; Vector: lambda zap; Site 1: EcoRI, Site 2: XhoI; total RNA extraction from NaCl(200mM) treated Thellungiella salsuginea by RNAgent kit(Promega); mRNA isolation by MESSAGEMAKER kit(GIECO), directional cDNA synthesis(EcoRI XhoI) by cDNA synthesis kit(STRATAGEN); the ZAP express library by GigapackIII Gold Cloning kit(STRATAGENE)"
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/dev_stage="seedling"
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/db_xref="taxon:72664"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1014 DTTKGAKTKTTKKGKTNWTKTKKCKKTGKRKGDAKKAAAAADDKKTDKARAKKKGKKKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 TCTGTTCTTAAGTACGTTCACAAGGATTCCGAAGGTAACGACGGTGAGTTGTTTTTGGGCT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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    Web : www.genoscope.cns.fr)

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                                                     ANTACTGTTGGTAAGTTCCAAATCTTCCACCAAGCAGCTGAAGAGTTTGTTATGT
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/db xref="taxon:7227"
/clone="BACR32D23"
/clone_lib="RPCI-98"
/note="end: TET3"

166 c 7 g 284 t 489
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                                                                                                                                                                                                                                                                                                                                                                                                     1519 TACTTTTTGGGTAACCTGAACAGATTGATCAAGGCCAAATGGTTGTGGGATCCTAACGAG
                                                                                                                                                                                                                                                                                                                               1579 ATCTTCACAAACAACAGTCTATCCCTACTAAACCTCTTAAGGAG 1623
                                                                                                                                                                                                                                                                                           144
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                                                                                                           WHE1777 C01 F01ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE1777 C01 F01, mRNA sequence. BF202701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and KhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV805562 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-43-G11
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Large scale analysis of Arabidopsis full-length cDNA (2002b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oono,Y., Sakurai,T., Carninci,P., Kawaı,J., 100n,m., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                 bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: BamHI; Site_2: SalI; subjected dehydration (1, 2, 5, 10, 24 hr) and cold (1, hr) treatments"

9 c 64 g 121 t
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germination to mature seeds"
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/db_xref="taxon:3702"
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BU013165.1
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QGJ3015.yg.abl QG_EFGHJ
QGJ3015, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                           Lactuca sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The structure and function of the expressed genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Olin Anderson
US Department of Agriculture,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Seaton,C.L. and Tong,J.C.
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Anderson, O.D., Chao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Area, Western Regional Research Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: BCORI; Site 2: XhoI; Plants were grown in the greenhouse. Whole Spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside, Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparations and DNA sequencing were performed Anderson lab (all other authors)."
78 c 125 g 82 t
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/tissue type="Spike before anthesis"
/dev stage="Adult plant"
/lab_host="E. coli SOLR"
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/db_xref="taxon:4565"
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                                                                                                                                                                                           mRNA linear EST 22-AUG-2002 serriola Lactuca sativa cDNA clone
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Best Local Similarity 60.2%;
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                                                                                                                                                                                                                                               1362 AGACTITTACGAGGAGATGTATGAGCCTTATGGTGGTGTTCCAGACCCTTAACA 1414
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig4252, see http://cgpdb.ucdavis.edu/
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Fax: 1-(530)-752-9659
                                                                                                                                                                                              AGAGGTCTACAAGAAGGTGCATGCAGCTATTCGTGCTGATCCAACCCCTAAGA 163
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//lab_host="E.coli"
//lab_host=
//lab_h
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/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGJ3015"
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Location/Qualifiers
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AAS06159

Primer hox8 used i PCR primer hox2b u Primer hox10 used Primer hox18 used PCR primer 8 used Primer hox6 used i Primer hox7 used i

Primer hox9 used i
PCR primer hox9a u
Primer hox19 used
PCR primer 9 used
PCR primer hox10b

primer 4 used

PCR primer hox6b u
PCR primer hox7a u
PCR primer hox15 used
Primer box17 used
Primer ByllI-NsiI
PCR primer 7 used
PCR primer 7 used
PCR primer hox2b used
PCR primer hox1b u
PCR primer hox1b u
PCR primer hox4 used i
PCR primer hox4 used i
PCR primer hox4 used i
PCR primer box10 u
PCR primer box10 u
PCR primer box10 used
PCR primer box10 used
PCR primer hox10 used i
PCR primer hox11 used
PCR primer hox11 used
PCR primer hox11 used
PCR primer hox11 used

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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   IJ
              AAS06173
AAF23590
AAZ94039
AAT76552
AAZ94026
AAS06168
AAZ94015
                                                                                                                                                                                                                                SUMMARIES
            Hexose oxidase (HO Chondrus cripus he Synthetic hexose o DNA encoding hexos Primer hox16 used PCR primer 6 used Primer hox5 used i Primer hox14 used
                                                                                                                                                                             Description
primer hox5a
RESULT 1
AASO6173
ID AASO6
XX AASO6
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                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS06173;
                                 24-NOV-1999;
                                                                    24-NOV-2000; 2000WO-IB01886
                                                                                                                                          WO200138544-A1
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                  Chondrus crispus.
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(DANI-) DANISCO AS.
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                                 99GB-0027801
                                                                                                                                                                       /*tag= a
/product= "Hexose reductase (HOX)"
/EC_number= "EC 1.1.3.5"
                                                                                                                                                                                                                           Location/Qualifiers
1..1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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ВP

AAS06165 AAZ94037

PCR primer 3 used Primer -SKL-sense Primer -SKL-antise

ALIGNMENTS

Result No.

a 0.0

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The sequence represents the coding sequence of synthetic hexose oxidase CC (D-hexose.02-oxireductase, EC 1.1.3.5), also referred to as HOX, gene. CC (D-hexose.02-oxireductase, EC 1.1.3.5), also referred to as HOX, gene. CC The native HOX gene was altered using site-directed mutagenesis in order to match the codon usage to known codon preferences of biotechnologically crelevant yeasts, such as Pichia sp., to facilitate high level production in these organisms. The invention involves a method for releasing a soluble or membrane associated intracellular protein of interest (POI) cc from a cell involving contacting a cell comprising a soluble or membrane cx soluble or membrane cassociated intracellular POI with a membrane extracting composition (I) cc and causing the POI to be released from the cell in a soluble form. The method is useful for releasing POI, such as an interleukin I receptor cc antagonist (II-1ra) which involves contacting a transformed cell comprising II-1ra with (I) and causing II-1ra to be released from the cc screening mutated cell, in a soluble form. The method is also useful for screening mutated cells or transformed cells producing elevated levels of intracellular POI. The method is used to release a POI for manufacturing food products, such as beverages, preparation of detergents, and in cc baking as a dough improving agent. The method obtains a fast, specific and economically efficient extraction of a soluble or membrane associated intracellular POI without the use of conventional cell disruption contacting cell extract contains less contaminating cl intracellular POI can be recovered from a eukaryotic host organism such careful contact of intracellular POI with the extracellular growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367695/38
P-PSDB; AAU02192.
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Zargahi MR;
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TCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTTGCCAGGTGGTTCCTGTTACTCC
                                                                                        GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTTCCGGTGACACCAACTGGGGT
                                                                                                                                                                              TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTTGGTT
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                                                                  GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTCCGGTGACACCAACTGGGGT
                                                                                                                                                   TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTGGTT
                                                                                                                                                                                                                                       GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1644;
Pred. No. 0;
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Best Local Similarity
Matches 1644; Conserv
                                                                                                                                                                                                                                         The present invention relates to a new anti-fouling composition. The composition involves a surface coating material, a hexose oxidase enzyme obtained from a marine organism and a substrate for the enzyme. The anti-fouling composition is useful as a coating formulated for treating a surface, e.g. outdoor wood work, external surface of a central heating system, or a hull of a marine vessel. It is also useful as an anti-fouling agent for marine structures exposed to
                                                                                                                                                                                                                                                                                                                                                                              New anti-fouling composition, useful as a coating for treating different surfaces, e.g. outdoor woodwork, external surface of central heating system, or a hull of a marine vessel
                                                                                                                                                                                                      Sequence 1644
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                                                                               Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that modified by at least one codon
                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexose oxidase; production; fermentation; synthetic; modification; prokaryote; eukaryote; ss.
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                  Wild type hexose
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                                               Claim 1; Page 25-27; 42pp; English
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and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% higher than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasible using this method. This is a much improved method which produces at least 250 mg enzyme per liter 10% higher

Sequence 1644 BP; 430 A; 344 C; 401 G; 469 T; 0 other;

Score 1632.8; Pred. No. 0;

BB

21; Length

1644;

GGTACCAACATCGATTTCGTTTACGTCGTTTACACTCCACAAGGTGCTTGTACTGCTTTG ATGGCTACTTTGCCACAAAAGGACCCAGGTTACATTGTTATTGACGTCAACGCTGGTACT CCAGACAAGCCTGACCCAAGATTGCCATCCATGAAGCAAGGTTTCAACAGAAGATGGATT CACACTGGTGGAGGTGGAGGTAACTTCGGTATTATCACCAAATACTACTTCAAGGATTTG CACACTGGTGGAGGTGGAGGTAACTTCGGTATTATCACCAAATACTACTTCAAGGATTTG TTGCCAGTCGATTGGTTATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGAC GTCGGTTTGGGTGGTCACATTGTCGGTGGAGGTGACGGTATTTTGGCCAGATTGCACGGT TCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTTGCCAGGTGGTTCCTGTTACTCC GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTTCCGGTGACACCAACTGGGGT GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTCCCGGTGACACCCAACTGGGGT TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTGGTT GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT CCAGACAAGCCTGACCCAAGATTGCCATGAAGCAAGGTTTCAACAGAAGATGGATT AATACTGTTGGTAAGTTCCAAATCTTCCACCAAGCAGCTGAAGAGTTTGTTATGTACTTG AGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTCAAGTTGGCTAGATGTGATTGGAAG AGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTCAAGTTGGCTAGATGTGATTGGAAG CCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACACTTCTCTTGGGACGGTTTCACT TCTGTTCTTAAGTACGTTCACAAGGATTCCGAAGGTAACGACGGTGAGTTGTTTTGGGCT TCTGTTCTTAAGTACGTTCACAAGGATTCCGAAGGTAACGACGGTGAGTTGTTTTGGGCT GTCGGTTTGGGTGGTCACATTGTCGGTGGAGGTGACGGTATTTTGGCCAGATTGCACGGT TCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTGCCAGGTGGTTCCTGTTACTCC TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATCATCAACGTTACTGGTTTGGTT ATGGCTACTTTGCCACAAAAGGACCCAGGTTACATTGTTATTGACGTCAACGCTGGTACT CCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACACTTCTCTTGGGACGGTTTCACT TTGCCAGTCGATTGGTTATCCGGTGTCGAAGTCGTCGTTAAGCCAGTCTTGACCGAAGAC 0: Mismatches 7; Indels <u>.</u> Gaps 540 540 360 180 180 120 840 780 780 720 720 660 660 600 600 480 480 420 420 360 300 300 240 240 120 60 60

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                                                                                       Hexose oxidase; Chondrus crispus; marine algae; recombinant; antimicrobial; antioxidant; food preparation; dairy product; beverage; animal feed; silage; sugar reduction; cosmetics; d
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                                                                                                                                                                                                                                                                                                                                             AAT76552;
                                                          toothpaste; dough;
                                                                                                                                                                                                               DNA encoding hexose oxidase, an antimicrobial/antioxidant agent.
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TACGAGGACTTCGTATTTGACGAATGCGTCAAGGCCATCATCAACGTCACTGGTCTCGTT

GACCGTGCTATGGAAAAGTGTTCTCCCGGTACAGTCAGGATCGTCTCTGGCGGCCATTGC GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT

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Chondrus crispus

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Best Local Similarity
Matches 1416; Conserv
                                                                                                                                   AAT76552 encodes hexose oxidase (HO) of the marine algae species (Chondrus crispus. HO is useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can be recombinantly produced in industrially appropriate quantities, and at a quality and purity level which renders the polypeptide suitable for industrial purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                       Recombinant production of polypeptide having hexose oxidase activity - used in food preparations as antibacterial and antioxidant agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                               Sequence 1801 BP; 441 A; 448
                                                                                                                                                                                                                                                                                                                                Claim 28;
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Page 103-104; 124pp; English.
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                                                                                                                                                                        TATGAGCCTTATGGTGGTGTTCCAGACCCTAACACTCAGGTTGAGAGTGGTAAAGGTGTT
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TATGGTGCCTTGGAACTTTACTTTTTGGGTAACCTGAACAGATTGATCAAGGCCAAATGG
                                                                                     TTTGAGGGATGCTACCTTCAACTACCCTGATGTTGACTTGAACAACTGGAAGAACGGTAAG
                                                                                                                                                                                                                                                          CAGGAAGAAGACAAGGATGCAGTTAACTTGAAGTGGATTAGAGACTTTTTACGAGGAGATG
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                                                               TTTGAGGGATGCTACTTCAACTACCCGGATGTGGACTTGAACAACTGGAAGAACGGCAAG
                                                                                                                                                  TATGAGCCGTATGGCGGGGTTCCAGACCCCCAACACGCAGGTGGAGAGTGGTAAAGGTGTG
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RESULT 5
AAZ94026 c
ID AAZ94026 c
XX AAZ94026;
XX AAZ94026;
XX Primer hox
XX Hexose oxi
KW Prokaryote
XX Synthetic.
OS Synthetic.
XX Synthetic.
XX Synthetic.
XX Synthetic.
YX IN EP1008651-
XX Synthetic.
YX Nucleic ac
PT oxidase cc
PT oxidase cc
PT oxidase cc
PT modified h
XX Synthetic.
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                                           δ
                                                                                                                                                                                                                                                                                        wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organism and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% higher than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasible using this method. This is a much improved method which produces at least 250 mg enzyme per liter of fermentation medium. Twenty-eight primers (See AAZ94018).

With codon usage possibly optimised for expression in P. pastoris were used to produce the synthetic hexose oxidase gene (See AAZ94039).
                                                                                                                         Matches 126;
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                         Sequence 126 BP; 33 A; 35 C; 23 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 22; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified by at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer hox16 used in production of synthetic hexose oxidase gene.
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                                        GCTCTTCTTCAGGTTGATATGTTCGGTGGTGAGATTCACAAGGTTGTTTTGGGATGCTACT
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   GCTCTTCTTCAGGTTGATATGTTCGGTGGTGAGATTCACAAGGTTGTTTGGGATGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                     Score 126; DB 21;
Pred. No. 8.5e-28;
                                                                                                                         Mismatches
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                                                                                                                                                  8.5e-28;
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                                                                                                                                                                                 Length 126;
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RESULT 6
ARSO6188/c
ID AASO61
XX HOX; s
KW HOX; s
KW FOOD m
KW D-hexo
XX Chondr
OS Chondr
OS Chondr
OS Synthe
XX JOHANS
PF 24-NOV
XX 24-NOV
XX AASO61
PF 24-NOV
XX DANIS
PF 24-NOV
XX AASO61
CC CALL GAR
CC AASO61
CC CALL GAR
                                                                                              cc hexose oxidate (D-hexose:02-oxireductase, EC 1.1.3.5), (also referred to cas HOX), gene. The native HOX gene was altered using site-directed cc mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as Pichia sp., to facilitate cc high level production in these organisms. The invention involves a method cc for releasing a soluble or membrane associated intracellular protein of cc interest (POI) from a cell involving contacting a cell comprising a cc soluble or membrane associated intracellular POI with a membrane cell composition (I) and causing the POI to be released from the cell composition (I) and causing the POI to be released from the call intracellular POI and causing the POI such as an interleukin I receptor antagonist (II-Ira) which involves contacting a cell composition (I) and causing FOI. The method is also considered cell comprising II-Ira with (I) and causing FOI. The method is also constituted cell comprising the POI. The method is useful for release a POI couseful for screening mutated cells or transformed cells producing cell-wated levels of intracellular POI. The method is used to release a POI combrane associated intracellular POI without the use of conventional cell disruption techniques. The resulting cell extract contains less contains such as yeast, before Jayosylation takes place. The method can be used to conventions less contains such as yeast, before Jayosylation takes place. The method can be used to contain the contact of intracellular poi without the use of conventions less contains such as yeast, before Jayosylation takes place. The method can be used to contain the contact of intracellular poi without the such as contains less contains such as yeast, before of contacts poi without the contains and contact of intracellular poi without the such as yeast, before plycosylation takes place. The method can be used to contain the contact of intracellular poi without the contains and contact of the place of the place of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the PCR primer 6 used to clone synthetic hexose oxidase (D-hexose:O2-oxireductase, EC 1.1.3.5), (also refe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johansen CL,
Zargahi MR;
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                                                                             prevent contact of intracellular POI with
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Best Local (
                          of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasible using this method. This is a much improved method which produces at least 250 mg enzyme per liter of fermentation medium. Twenty-eight primers (See AAZ94011-Z94038) with codon usage possibly optimised for expression in P. pastoris were used to produce the synthetic hexose oxidase gene (See AAZ94039)
                                                                                                                                                                              Wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organism and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% higher
                                                                                                                                                                                                                                                                                                  Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 126 BP; 33
                                                                                                                                                                                                                                                                                                                                                                           Stougaard P,
                                                                                                                                                                                                                                                     Example 2; Page 20; 42pp; English.
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                                                                                                                                                than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-389309/34
                                                                                                                                                                                                                                                                                                                                                                                                         (BIOT-) BIOTEKNOLOGISK INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prokaryote;
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                                                                                                                                                                                                                                                                                    at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eukaryote; ss.
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                                                                                                                                                                                                                                                                                    least one
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                                                                                                                                                                                                                                                                                                                                                                             Wolff AM,
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Pred. No. 8.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 G;
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Query Match Best Local Similarity

100.0%; 7.3%;

Score 120; DB 21; Pred. No. 5.4e-26;

Length 120

Sequence 120

BP; 26 A; 26 C; 31 G; 37 T; 0 other;

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TCCGGTGACACCAACTGGGGTTCCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTG

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AATCAGAGAGGTAAGTACAAGTCTGCTTACATGATCAAGGACTTTCCAGACTTCCAGATT 1
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RESULT 9
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HOX; seaweed; hexose oxidase; interleukin I receptor antagonist; food manufacturing; beverage; detergent; baking; dough improving D-hexose:02-oxireductase; EC 1.1.3.5; PCR primer; hox5a; ss. IL-lra;
agent;

PCR primer hox5a used to clone synthetic HOX

gene

WO200138544-A1 Chondrus crispus

31-MAY-2001

24-NOV-2000; 2000WO-IB01886

24-NOV-1999; 99GB-0027801

(DANI-) DANISCO AS

Kjaerulff ŝ Madrid SM, Pedersen Ħ, Poulsen 9

WPI; 2001-367695/38

Releasing soluble or membrane associated intracellular protein from a cell for manufacturing food, comprises contacting the cell with a membrane extracting composition and causing the protein to be released in soluble form with a be released

Claim 19; Fig 5; 108pp; English

The sequence represents the PCR primer hox5a used to clone synthetic CC as HOX), gene. The native HOX gene was altered using site-directed CC as HOX), gene. The native HOX gene was altered using site-directed CC mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as pichia sp., to facilitate high level production in these organisms. The invention involves a method CC for releasing a soluble or membrane associated intracellular protein of CC interest (POI) from a cell involving contacting a cell comprising a CC extracting composition (I) and causing the POI with a membrane cell in a soluble form. The method is useful for releasing POI, such as transformed cell comprising II-lra with (I) and causing IV-lra to be creleased from the transformed cell, in a soluble form. The method is also useful for screening mutarted cells or transformed cells producing celevated levels of intracellular POI. The method is used to release a POI for manufacturing food products, such as beverages, preparation of detergents, and in baking as a dough improving agent. The method obtains cell disruption techniques. The resulting cell extract contains less contaminating intracellular POI without the use of conventional contaminating intracellular POI without the use of conventional contaminating such as yeast, before glycosylation takes place. The method can be used to prevent contact of intracellular POI with the extraction of contaminating intracellular POI can be recovered from a eukaryotic host organism such as yeast, before glycosylation takes place. The method can be used to prevent contact of intracellular POI with the extractellular POI with the extracellular POI with the extr

Sequence 120 BP; 26 A; 26 C; 31 G; 37 T; 0 other;

Query Match Best Local Similarity 100.0%; 7.3%; Score 120; DB 22; Pred. No. 5.4e-26; Length 120;

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                                                    for releasing a soluble or membrane associated intracellular protein of interest (POI) from a cell involving contacting a cell comprising a soluble or membrane associated intracellular POI with a membrane extracting composition (I) and causing the POI to be released from the cell in a soluble form. The method is useful for releasing POI, such as an interleukin I receptor antagonist (II-Ira) which involves contacting a transformed cell comprising II-Ira with (I) and causing II-Ira to be released from the transformed cell, in a soluble form. The method is also useful for screening mutated cells or transformed cells producing elevated levels of intracellular POI. The method is used to release a POI for manufacturing food products, such method is used to release a POI for manufacturing food products, such method is used to release a fast, specific and economically efficient extraction of a soluble or membrane associated intracellular POI without the use of conventional
                                                                                                                                                                                                                                                                                                                     The sequence represents the PCR primer 4 used to clone synthetic hexose oxidase (D-hexose:O2-oxireductase, EC 1.1.3.5), (also referred to as HOX), gene. The native HOX gene was altered using site-directed mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as Pichia sp., to facilitate high level production in these organisms. The invention involves a method
cell disruption techniques. The resulting cell extract contains less contaminating intracellular DNA and is relatively free of cell wall fragments. The intracellular POI can be recovered from a eukaryotic host
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Fig 5; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Releasing soluble or membrane associated intracellular protein from a cell for manufacturing food, comprises contacting the cell with a membrane extracting composition and causing the protein to be released in a label for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOX; seaweed; hexose oxidase; interleukin I receptor antagonist; IL-1ra; food manufacturing; beverage; detergent; baking; dough improving agent; D-hexose:O2-oxireductase; EC 1.1.3.5; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367695/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zargahi MR;
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ARESULT 11
ARZ94019
ID ARZ944019
AC ARZ94
XX ARZ94
XX ARZ94
XX Prime
XX Hexos
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DE Prime
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Best Local
                                                       than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasible using this method. This is a much improved method which produces at least 250 mg enzyme per liter of fermentation medium. Twenty-eight primers (See hAZ94011-Z94038) with codon usage possibly optimised for expression in P. pastoris were used to produce the synthetic hexose oxidase gene (See AAZ94039)
                                                                                                                                                                                                                                                                                                                                                                           Wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organic and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that modified by at least one codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth medium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 120 BP; 33 A; 25 C; 29 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 21; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stougaard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexose oxidase; production; fermentation; synthetic; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer hox9 used in production of synthetic hexose oxidase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DK-0001630
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                                                                                                                                                                                                                                                                                                                                                                                                                                      an organism
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Query Match Best Local Similarity

100.0%; 7.2%;

Score 118; Pred. No.

DB 21; 2.1e-25;

Sequence 118

BP; 30 A; 27 C; 22 G;

39 T; 0 other;

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RESULT 12
AASO6
XX AASO6
XX ASO6
XX ASO6
XX ASO6
XX FOR P
XX HOX;
XW Food
XW D-hex
XX D-hex
XX D-hex
XX ASO6
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The sequence represents the PCR primer hox9a used to clone synthetic CC hexose oxidase (D-hexose:O2-oxireductase, EC 1.1.3.5), (also referred to CC as HOX), gene. The native HOX gene was altered using site-directed CC mutagenesis in order to match the codon usage to known codon preferences CC of biotechnologically relevant yeasts, such as Pichia sp., to facilitate CC high level production in these organisms. The invention involves a method CC for releasing a soluble or membrane associated intracellular protein of CC interest (POI) from a cell involving contacting a cell comprising a CC soluble or membrane associated intracellular POI with a membrane CC extracting composition (I) and causing the POI to be released from the CC cell in a soluble form. The method is useful for releasing POI, such as CC transformed cell comprising II-1ra with (I) and causing II-1ra to be CC useful for screening mutated cell, in a soluble form. The method is useful for membrane associated levels of intracellular POI. The method is used to release a POI CC detergents, and in baking as a dough improving agent. The method obtains a fast, specific and economically efficient extraction of a soluble or cell disruption techniques. The resulting cell extract contains less contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host contaminating intracellular POI can be recovered from a eukaryotic host can be seen contaminating intracellular POI can be recovered fro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS06161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS06161 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in soluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCTCTTGGGACGGTTTCACTAGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAATACTACTTCAAGGATTTGCCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATACTACTTCAAGGATTTTGCCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCTCTTGGGACGGTTTCACTAGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 5; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kjaerulff S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99GB-0027801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madrid SM, Pedersen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poulsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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RESULT 13
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ID AAZ944029
AC AAZ94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                  that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasing this method. This is a much improved method which produces at least 250 mg enzyme per liter of fermentation medium. Twenty-eight primers (See AAZ94011-Z94038) with codon usage possibly optimised for expression in P. pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism such as yeast, before glycosylation takes place. The method cobe used to prevent contact of intracellular POI with the extracellular
                                                                                                                                                                                                                                                                                                expressed, under identical conditions, at a level at least 10% higher than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods
                                                                                                                                                                                                                                                                                                                                                                                      Wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organism and modifying the sequence so that the modified sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid fragment useful for producing oxidase comprises nucleotide sequence encommodified by at least one codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118 BP;
                                                                                                                                                                                                                                                                        of producing hexose oxidase were to isolate the enzyme from a source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 23; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-389309/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1008651-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prokaryote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexose oxidase; production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer hox19 used in production of synthetic hexose oxidase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ94029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-) BIOTEKNOLOGISK INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAATACTACTTCAAGGATTTGCCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAATACTACTTCAAGGATTTGCCAATGTCTCCAAGAGGTGTCATCGCTTCTAACTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCTCTTGGGACGGTTTCACTAGAGATGCCTTGCAAGATTTGTTGACTAAGTACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                             produce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pedersen LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98DK-0001630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0204068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                             synthetic hexose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fermentation; synthetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolff AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ucing large amounts of hexose encoding hexose oxidase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poulsen U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                oxidase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modification;
                                                                (See AAZ94039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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Query Match Best Local Similarity

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7.1%;

Score Pred.

117; . No.

DB 21; 4.3e-25;

Length 117

Sequence 117

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A; 23 C;

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32 T; 0 other;

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The sequence represents the PCR primer 9 used to clone synthetic CC hexose oxidase (D-hexose:O2-oxideate, EC 1.1.3.5), (also referred to CC as HOX), gene. The native HOX gene was altered using site-directed CC mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as Pichia sp., to facilitate high level production in these organisms. The invention involves a method CC for releasing a soluble or membrane associated intracellular protein of CC interest (POI) from a cell involving contacting a cell comprising a Soluble or membrane associated intracellular POI with a membrane associated intracellular POI to be releasing POI, such as cell in a soluble form. The method is useful for releasing POI, such as creaming cell comprising II-1ra with (I) and causing II-1ra to be consisted from the transformed cell, in a soluble form. The method is also CC released from the transformed cell, in a soluble form. The method is used to release a POI for manufacturing food products, such as beverages, preparation of a fast, specific and economically efficient extraction of a soluble or cell disruption techniques. The resulting cell extract contains less contaminating intracellular POI can be recovered from a eukaryotic host fragments. The intracellular POI can be recovered from a eukaryotic host
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D-hexose:02-oxireductase; EC 1.1.3.5; PCR primer; ss.
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The sequence represents the PCR primer hox10b used to clone synthetic CC hexose oxidase (D-hexose:O2-oxireductase, EC 1.1.3.5), (also referred to CC as HOX), gene. The native HOX gene was altered using site-directed CC mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as Pichia sp., to facilitate CC high level production in these organisms. The invention involves a method CC for releasing a soluble or membrane associated intracellular protein of CC interest (POI) from a cell involving contacting a cell comprising a CC soluble or membrane associated intracellular poI with a membrane CC extracting composition (I) and causing the POI to be released from the CC cell in a soluble form. The method is useful for releasing POI, such as CC an interleukin I receptor antagonist (II-1ra) which involves contacting a CC transformed cell comprising II-1ra with (I) and causing II-1ra to be creleased from the transformed cell, in a soluble form. The method is also cuseful for screening mutated cells or transformed cells producing
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Pred. No. 4.3e-25;
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8 g 밁 ş Query Match 7.1%; Score 116.4; DB 22; Length 118; Best Local Similarity 99.2%; Pred. No. 6.5e-25; Matches 117; Conservative 0; Mismatches 1; Indels 0; elevated levels of intracellular POI. The method is used to release a POI for manufacturing food products, such as beverages, preparation of detergents, and in baking as a dough improving agent. The method obtains a fast, specific and economically efficient extraction of a soluble or membrane associated intracellular POI without the use of conventional cell disruption techniques. The resulting cell extract contains less contaminating intracellular DNA and is relatively free of cell wall fragments. The intracellular DNA and is relatively free of cell wall fragments the intracellular POI can be recovered from a eukaryotic host organism such as yeast, before glycosylation takes place. The method can be used to prevent contact of intracellular POI with the extracellular growth medium. Sequence 118 BP; 39 A; 26 C; 20 G; 33 T; 0 other; 0; Gaps 0

Search completed: June 15, 2003, 02:56:53 Job time: 389 secs

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Database :
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have

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SUMMARIES

#### Result No. 1638 1280.8 1279.2 1279.2 117 116.4 116 111 109 109 108 108 107 108 107 56.8 56 43.6 42.6 42.6 92.8 85.4 85.4 85.2 81.8 79.6 77.2 999999 Query Match 100 99 77 77 77 24225 215050 25883 26195 10668 214050 90 Length 45624 50000 80161 80161 2088 1141 1738 1738 89473 1639 1785 51939 91566 1620 DB AX155104 CCU9979 AR15972 AR15972 AR155099 AX155099 AX155097 AX155097 AX155091 AX155091 AX155091 AX155090 AX155095 AX155096 AX1550 AL646057 AB008466 SC1G7 AX155103 AX089430 AX089416 AX009416 AX105018 SPUB0222 AX155084 AY007564 AY107564 AY107564 AY107508 AX15084 AY0751000 TIK7 AX15083744 AY0751000 TIK7 AX113892 AX155104 Sequence AX294935 Synthetic U89770 Chondrus cr AR159722 Sequence AX155098 Sequence AX155098 Sequence AX155097 Sequence AX155093 Sequence AX155093 Sequence AX155093 Sequence AX155093 Sequence AX155090 Sequence AX155090 Sequence AX155090 Sequence AX155098 Sequence AX155096 Sequence AX155096 Sequence AX155097 Reguence AX155098 Sequence U80222 Streptomyce AX155084 Sequence AX083744 Sequence AY051000 Arabidops AC013427 Sequence AY113892 Arabidops AF360332 Arabidops AC099341 Homo sapi AC007296 Arabidops Description

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TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX155104	RESULT 1
Poulsen,C.H. and Zargahi,M.R. Method for purifying proteins Patent: WO 0138544-A 22 31-MAY-2001;	Johansen, C.L., kj Rulff, S.R., Madrid, S.M., Pedersen, H.,	1 (bases 1 to 1644)	artificial sequences.	synthetic construct	synthetic construct.	•	AX155104.1 GI:14536652	AX155104	Sequence 22 from Patent	AX155104 1644 bp DNA linear PAT		
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CAGTCGATTGGTTATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGAC 540	TTGCCAGTCGATTGGTTATCCGGTGTTGAAGTTGTCGTTAAGCCAGTCTTGACCGAAGAC 540	GTCGGTTTGGGTGGTCACATTGTCGGTGGAGGTGACGGTATTTTGGCCAGATTGCACGGT 480	CCTTCAAGACCTTGTTCAGAGACCACGGTAGAGTTTTGCCAGGTGGTTCCTGTTACTCC 420	GAATCTGGTTACGACGACGATAGAGGTTACTTCGTCTCTTCCGGTGACACCAACTGGGGT 360	TACGAAGACTTCGTTTTCGACGAATGTGTCAAGGCTATTATCAACGTTACTGGTTTGGTT 300	GACAGAGCTATGGAAAAGTGTTCTCCAGGTACCGTCAGAATCGTTTCTGGTGGTCACTGT 240	GGTACCAACATCGATTTCGTTTACGTCGTTTACACTCCACAAGGTGCTTGTACTGCTTTG 180	CCAGACAAGCCTGACCCAAGATTGCCATCCATGAAGCAAGGTTTCAACAGAAGATGGATT 120	AAGGACCCAGGTTACATTGTTATTGACGTCAACGCTGGTACT 60	99.6%; Score 1638; DB 12; Length 1638; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGKYGALELYF LGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLKEPKQTK" 337 c 402 g 471 t	DLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEF WYLYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGHAGWAPFPVRFPKRH YSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIVIKYLTEV PDGLTSAEWKDALLOVDMFGGEIHKVYWDATAVAOREYIKKOYOTYWOEEPKDANVI	/translation="MATLPQKDPGYIVIDVNAGTPDKPDPRLPSMKQGFNRRWIGTNI /translation="MATLPQKDPGYIVIDVNAGTPDKPDPRLPSMKQGFNRRWIGTNI DFVYVVYTPQGACTALDRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVES GYDDDRGYFVSSGDTNWGSFKTLFRDHGKTVLPGGSCSVSUGLGAIIVCGGDGILARLIG LBLNWISGSFKYNFRDSVT.XVIJKNEGGNOEFFFANTGCGCGNGTTTTXYVEK	/trans1 table=11 /trans1 table=11 /product="hexose oxidase" /product="hexose oxidase" /protein id="CAC12830.1" /h vrof="[CT.10736666"]	equenc aa seg =1	/gene="sHOX" /ge.ne="sHOX" /ge.ne="sHOX" /ge.ne="sHOX"	/db_xref="taxon:32630" /note="Chondrus crispus sequence with codon usage optimized to Pichia pastoris" 11638	Location/Qualifiers 11638 /organism="synthetic construct"
Ş	B 8	Db 49	S B &	D &	S B S	D 09	Qγ bb	עס da	D Qy	Qу	Qy Db	οδ	g &	B 8	D Qy	Qy Db	Qy db	Qy Db
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Stougaard, P. and Hansen, O.C.
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1 (bases 1 to 1881)

Hansen,O.C. and Stougaard,P.

Hexose oxidase from the red alga Chondrus crispus. Phelocular cloning, and expression in Pichia pastoris J. Biol. Chem. 272 (17), 11581-11587 (1997)
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GLPUDWLSGVEVVKPVLTEDSVLKYVHKDSEGNDGELFWAHTGGGGNFGIITKYYFK
DLPMSPRGVIASNLHFSWDGFTRALQDLTKYFKTLARCDMKNTVGKFQIFHQAAEEF
VMYLYTSYSUNDAFETVADDFHYHLEADIEQIYKTCEPTKALGGHAGMAPFPKFPKKH
TSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEV
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OV 301 CHARCTOGETHACCACCANADAGGETHACTTOTTCACCANGTOCACTOCACTOCACTOCACTOCACTOCACTOCACTOCA	Query Match Best Local Similarity 86.1%; Pred. No. 0; Matches 1416; Conservative 0; Mismatches 228; Indels 0; Gaps 0; Matches 1416; Conservative 0; Mismatches 228; Indels 0; Gaps 0;  Qy 1 ATGGCTACTTTGCCACAAAAGGACCCAGGTTACATTGTATTGACGTCAACGCTGGTACT 60	such enzyme Patent: EP 1020523-A 30 19-JUL-2000; BIOTEKOLOGISK INST (DK)  Location/Qualifiers 1. 1801  /organism="unidentified" /db_xref="taxon:32644"  84. 1724  /note="unnamed protein product" /codon_start=1 /codon_start=1 /protein_id="CAC09603.1" /db_xref="gi:10278112"  /db_xref="gi:10278112"  /db_xref="gi:10278112"  /db_xref="gi:10278112"  /protein_id="CAC09603.1" /protein_id="CAC09603.1" /protein_id="CAC09603.1" /protein_id="CAC09603.1" /protein_id="CAC09603.1" /protein_id="CAC09603.1" /db_xref="gi:10278112"  /db_xref="gi:10	Db 1584 TATGGTGCCCTCGAACTTTACTTTTTGGGTAACCGCCTCATCAAGGCCAAATGG 1643  Qy 1561 TTGTGGGATCCTAACGAGATCTTCACAAACAACAGTCTATCCCTACTAAACCTCTTAAG 1620
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1 (bases 1 to 126)
Johansen, C.L., kj Rulff, S.R., Madrid Poulsen, C.H. and Zargahi, M.R.
Method for purifying proteins
Patent: WO 0138544-A 17 31-MAY-2001;
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 120)
                                                                      Sequence 6 from Patent WO0138544. AX155088
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                                                                                                                                                                                 GACAAG 1335
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/db xxef="taxon:32630"
/note="Synthetic oligonucleotide"
35 c 23 g 35 t
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WO0138544.
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RESULT 9
AX155092
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AX155097/c
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Best Local Simi
Matches 120;
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Best Local Similarity
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Sequence 10
AX155092
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synthetic construct. synthetic construct artificial sequences
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1 (bases 1 to 120)
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/db xxef="taxon:32630"
/note="Synthetic oligonucleotide"
/s c 29 g 33 t
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/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
26 c 31 g 37 t
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from Patent WO0138544.
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Pred. No. 5.1e-21;
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Pred. No. 5.1e-21;
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AX155102
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AX155093/c
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Johansen, C.L., kj Rulff, S.R., Madrid, S.M.,
Poulsen, C.H. and Zargahi, M.R.
Method for purifying proteins
Patent: WO 0138544-A 10 31-MAY-2001;
DANISCO A/S (DK)
 synthetic
synthetic
                                              AX155093
Sequence 11 from Patent
AX155093
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Johansen, C.L., kj Rulff, S.R., Madrid
Poulsen, C.H. and Zargahi, M.R.
Method for purifying proteins
Patent: WO 0138544-A 20 31-MAY-2001,
DANISCO A/S (DK)
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Sequence 20 from Patent
AX155102
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synthetic construct
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llarity 100.0%; Pred. No. 3.3e-20;
Conservative 0; Mismatches 0;
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/db xxef="taxon:32630"
/note="Synthetic oligonucleotide"
27 c 22 g 39 t
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23 c 26 g 32 t
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/db_xref="taxon:32630"
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                                     GI:14536641
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AX155091/c
LOCUS
                                   RESULT 13
AX155101/c
LOCUS
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Best Local Simi
Matches 116;
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                     Sequence 19
AX155101
AX155101.1
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Sequence 9 1
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AX155091.1
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1 (bases 1 to 118)
Johansen, C.L., kj Rulff, S.R., Madrid Poulsen, C.H. and Zargahi, M.R.
Method for purifying proteins
Patent: WO 0138544-A 11 31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                    Johansen,C.L., kj Rulff,S.R., Madrid,S. Poulsen,C.H. and Zargahi,M.R. Method for purifying proteins Patent: WO 0138544-A 9 31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequences.
1 (bases 1 to 116)
                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct.
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/db xref="taxon:32630"
/note="Synthetic oligonucleotide"
31 c 22 g 30 t
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26 c 20 g 33 t
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Pred. No. 4.8e-20;
0; Mismatches 1;
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Pred. No. 6.1e-20
0; Mismatches (
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JOURNAL
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Best Local Similarity 100.0%; I
Matches 109; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 109)
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1 (bases 1 to 111)
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/db_xref="taxon:32630"
/note="Synthetic ooligonucleotide"
38 c 20 g 16 t
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/db_xref="taxon:32630"
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30 c 21 g 30 t
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from Patent WO0138544.
    GI:14536638
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Pred. No. 1.4e-18;
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                 completed: June 15,
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1 (bases 1 to 109)

Johansen, C.L., kj Rulff, S.R., Madrid, S.M.,

Poulsen, C.H. and Zargahi, M.R.

Method for purifying proteins

Patent: WO 0138544-A 8 31-MAY-2001;

DANISCO A/S (DK)
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Conservative (
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23 c 28 g 36 t
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Pred. No. 4.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
Published_Applications_AA:*

1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*
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2997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392085 seqs, 103240269 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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91.5	91.5	91.5	92	92	94	94	95	95	96.5	107	263	266	272	275	277	292.5	2989	2997	Score
<u>د</u> .	υ - μ	3.1	3.1	3.1	3.1	3.1	3.2	3.2	3.2	3.6	8.8	8.9	9.1	9.2	9.2	9.8	99.7	100.0	Query Match Length DB
85.	550	413	589	584	657	600	657	622	254	19	508	540	529	529	508	509	546	546	ength
v	o o	9	10	10	10	φ	10	9	9	10	9	9	9	ø	ø	9	10	10	DB.
0S-10-011-588-25	US-09-738-626-5417	US-09-910-186A-22	US-09-815-242-10878	US-09-815-242-5013	US-09-815-242-13013	US-10-234-026-13	US-09-815-242-12135	US-10-124-880-4	US-09-880-748-1466	US-09-932-923-1	US-09-258-031B-71	US-09-258-031B-58	US-09-258-031B-20	US-09-258-031B-16	US-09-258-031B-73	US-09-258-031B-75	US-09-824-053-31	US-09-998-284-2	ID
Sequence 25, Appl	Sequence 5417, Ap	Sequence 22, Appl	Sequence 10878, A	Sequence 5013, Ap	Sequence 13013, A	Sequence 13, Appl	Sequence 12135, A	Sequence 4, Appli	Sequence 1466, Ap	Sequence 1, Appli	Sequence 71, Appl	Sequence 58, Appl	Sequence 20, Appl	Sequence 16, Appl	Sequence 73, Appl	Sequence 75, Appl	Sequence 31, Appl	Sequence 2, Appli	Description
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5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
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US-09-738-626-6444	US-09-880-748-1545	US-10-108-605-103	US-10-118-495-29	US-09-829-378-2	US-09-911-842-2	US-10-150-821-2	US-10-234-026-15	US-08-325-278-3	US-08-325-278-1	US-09-782-906-4	US-09-782-906-3	US-10-032-717-2	US-10-007-693-95	US-09-880-748-1153	US-09-782-906-5	US-09-782-906-2	US-10-011-366-10	US-10-011-366-21	US-10-011-366-20	US-09-801-196-20	US-09-759-130B-176	US-09-824-053-9	US-09-824-053-2	US-09-841-132-329	
Sequence 6444, Ap	Sequence 1545, Ap	Sequence 103, App	Sequence 29, Appl	Sequence 2, Appli		Sequence 2, Appli	Sequence 15, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 95, Appl	Sequence 1153, Ap	-	Sequence 2, Appli	-		Sequence 20, Appl	Sequence 20, Appl	Sequence 176, App	Sequence 9, Appli	Sequence 2, Appli	Sequence 329, App	Je

# ALIGNMENTS

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Sequence 2, Application US/09998284

Patent No. US20020106361A1

GENERAL INFORMATION:

APPLICANT: POULSEN, et al.

TITLE OF INVENTION: COMPOSITION

FILE REFERENCE: 674509-2035

CURRENT APPLICATION NUMBER: US/09/998,284

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: PCT/IB00/00829

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: GB 9913050.2

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 546

TYPE: PRT

ORGANISM: Chondrus crispus

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US-09-998-284-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Matches
                        181 SVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFT 240
                                                                        121
                                                                                            121 SFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTED 180
181
                                                                                                                                                                                                                                                                                                            546;
                                                                                                                                                                             61 DRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWG
                                                                                                                                                     61 DRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWG
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                                                                                                                                                                                                                                  1 MATLPQKDPGYIVIDVNAGTPDKPDPRLPSMKQGFNRRWIGTNIDFVYVVYTPQGACTAL
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                                                                                                                                                                                                                                                                                                                                               Length 546;
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                                               US-09-824-053-31
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              Query Match
 Best Local Similarity
                                                                                                                                       TELEX: NO. US20020106725A1e INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                    NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: <UI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/824,053
FILING DATE: 03-Apr-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,304
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Peter Stougaard
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                                                                                                            TYPE: amino acid
                                                                                                                                                                                        TELEPHONE: (202) 955-19
TELEFAX: (202) 778-2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hunton & Williams STREET: 1900 K Street, N.W.
                                                                                                                          LENGTH: 546 amino acids
 99.7%;
Score 2989;
Pred. No. 1
                                                                                                                                                                                                                                          <Unknown>
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1.9e-261;
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EPKQTK 546
                                                                                                                                                                             DATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEFYGGVFDPNTQVESGKGV
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                                      EPKQTK 546
                                                                                                   FEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLI KAKWLWDPNEI FTNKQSI PTKPLK
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                                                                             FEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK
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RESULT 3
US-09-258-0318-75
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COUNTRY: USA
ZIP: 10023 - 7604
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MINDOWS 95
SOFTWARE: WORDPERFECT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: NEW YORK
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STREET: 26
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PONSTEIN, Anne .

LAGEWEG, Wessel

PONSTEIN, Anne Silene
ANTIFUNGAL PROTURE ANTIFUNGAL PROTURE ANTIFUNGAL PROTURE ANTIFUNGAL PROTURE 
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26 WEST 61 STREET
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CUSTERS, Jerome Humbertina Hens
SELA-BUKLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna P.
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US-09-258-031B-73
Sequence 73, Application US/09258031B
Fatent No. US20020168735A1
GENERAL INFORMATION:
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                                                         APPLICANT:
APPLICANT:
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APPLICATION NUMBER: EP97:
FILING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/04923
FILING DATE: 04-SEP-1997
                   APPLICANT:
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  APPLICANT:
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                                                                                                                                                                                                                                                              486 VKIKTKVDPENFFRHEQSIPPMP 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 DRAAMGED--LFWAIRGGGGASFGIVLAWKIKLVPV-PKTVTVFTV-----TKTLEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 HKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 KSKIHGFPAGLCTSVGIGGYMTGGGYGTLMRKYGLAGDNVLDVKMV------DANGKLL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 HGRV--LPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 RVRSGGHDFEALSYVSRIEKPFILLDLSKLKQINVDIESNSAWVQPGAT-LGELYYRIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 RIVSGGHCYEDFVFDECVK---AIINVTGLVESGYD-DDRGYFVSSGDTNWGSFKTLFRD 128
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nilarity 24.9%;
Conservative 6
            STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BURLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna Pieternella
LAGEWEG,
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25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KATSDFVKEPIPVIGFKGIFKRLIE---GNTT-----
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Pred. No. 6.4e-18;
8; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GGHAGWAPFPVRPRKRHTSKTSYMHDE 344
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APPLICATION NUMBER: PCT/EP97/04923
FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP97200831.2
FILING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP96202466.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-SEP-1996 INFORMATION FOR SEQ ID NO: 7
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: J.25" Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS 95 CONTWARE: WORDPERFECT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                            342
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                                                                                                                                                                                                   289 MFLGDTTTLLSILNRRF---PELGLVRSDCTETSWIQSVLFWTNIQVGSSE--
                                                                                                                                                                                                                                                                                 241 LEQNATDIIH------RWQQVAPKLPDELFIRTVIDVVNGTVSSQKTVRTTFIA
                                                                                                                                                                                                                                                                                                                                                                                                        176 VLTEDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFS
461 YEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLN-NWKNGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 DTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 VRIVSGGHCYED-----FVFDECVKAIINV----TGLVESGYDDDRGYFVSSG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 MKIRSGGHDYDGLSYVTYSGKPFFVLDMFNLRSVDVDVASKTAWVQTGAILGEVYYYI---
                                                                                                                                                                                                                                                                                                                                                                ----DVNGKILDRKLMGED--LYWAINGGGGGSYGVVLAYKI-NLVEVPENVTVFRISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---WEKSKTL-----AYPAGICPTVGVGGHISGGGYGNWMRKYGLTVDNTIDARMV---
                                                                            KDALLQVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEM
                                                                                                                                                        HDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEM 401
                                                                                                                                                                                                                                                                                                                     WDGFTRDALQDLLTKYFKLARCDWKNTVGKF--QIFHQAAEEFVMYLYTSYSNDAEREVA
                                    EIPTMAFNPYGGEMGRISSTVTPFPYRAGNLWKIQYGANWRDETLTDRYMELTRKLYQFM
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VENTION: ANTIFUNGAL PROTEINS, DNA CODING
VENTION: THEREFOR, AND HOSTS INCORPORATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                    ---TILLORNOPVNYLKRKSDYVREPISRTGLESIWKKM-----IEL
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Pred. No. 1.6e-16;
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Length 508; Indels 122;

Gaps

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US-09-258-031B-16
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-SEP-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
TITLE OF IN
TITLE OF IN
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FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP972
FILING DATE: 19-MAR-1997
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                                                                                                                                                                                                                                                                                TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERFECT 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,031B
FILING DATE: 25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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MEDIUM TYPE: 3.25" F
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
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                                                                                                                                                                                                                                                                                                               amino acid
SGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGL 161
                                                    GKQNRLLLKTR-----SGGHDYEGLSYLTNTNQPFFIVDMFNLRSINVDIEQETAWVQ 146
                                                                                         TALDRAMEKCSPGTVRIVSGGHCYED----
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                                                                                                                         DRADPSFPITGEVYTPGNSSFPTVLQNYIRNLRFNETTTPKPFLIITAEHVSHIQAAVVC 93
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LAGEWEG, Wessel
PONSTEIN, Anne Silene
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VAN DEVENTER-TROOST, Johanna
                                                                                                                                                                                              Conservative
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CUSTERS, Jerome Humberti
                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                          EP96202466.7
                                                                                                                                                                                             64; Mismatches 197; Indels 198;
                                                                                                                                                                                                               Score 275; DB 9;
Pred. No. 2.6e-16;
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                                                                                       -----FVFDECVKAIINV----TGLVE 101
                                                                                                                                                                                                                                 DB 9;
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Patent No. US20020168735A1
                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.25" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PONSTEIN, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                    FILING DATE: 25-FEB-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                   APPLICATION NUMBER: PCT/EP97/04923 FILING DATE: 04-SEP-1997
                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10023 - 7604
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STREET: 26 WEST 61 STREET
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LAGEWEG, Wessel
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                                                                                       25-FEB-1999
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Jerome Humbertina Henricus Victor
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US-09-258-031B-58
, Sequence 58, Application US/09258031B
, Patent No. US20020168735A1
, GENERAL INFORMATION:
, APPLICANT: STUTVER, Maarten Hendri
APPLICANT: CUSTERS, Jerome Humbert
, APPLICANT: SELA-BURLAGE, Marianne
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Best Local Similarity
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                  APPLICANT:
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LENGTH: 529 amino acid
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APPLICATION NUMBER:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              424 AVAQRE-YIIKLQYQTYWQEEDKDAVN--LKWIRDFYEEMYEPYGGVPDPNTQVESGKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 GKQNRLLLKTR-----SGGHDYEGLSYLTNINQPFFIVDMFNLRSINVDIEQETAWVQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 DRADPSFPITGEVYTPGNSSFPTVLQNYIRNLRENETTTPKPFLIITAEHVSHIQAAVVC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQVDMFGGEIHKVVWDAT
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                                                                                                                                                                                                                                                                                                                               -REAFLNYRDLDIGINSHGRNAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFFRNEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSYMHDE-----TMDYPFYALTE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVPEVVTV-------FTIERREEQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVDNIVDAQII-----DVNGKLLDRKSMGED--LFWAITGGGGVSFGVVLAYKIK-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATLGEVYYRIAEKSN-----KHG--FPAGVCPTVGVGGHFSGGGYGNLMRKYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TALDRAMEKCSPGTVRIVSGGHCYED------FVFDECVKAIINV-----TGLVE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKPDP------RLPSMKQGF--NRRWIGTNIDFVYVVYTPQG-----AC
                                                                                                                                                                                                                                                    IPT 526
                                                                                                                                                                                                                                                                                          IPT 536
                                                                                                                                                                                                                                                                                                                                                                   FEGCYFNYPDVDLNNWKNGKYGALELYFLG-----NLNRLIKAKWLWDPNEIFTNKQS
                                                                                                                                                                                                                                                                                                                                                                                                       PFPHRSGNIAKIQYEVNWEDLSDEAENRYLNFTRLMYDYMTPFVSKNP----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLYLGNSRNLVTLLNKDFPELGLQESDCTEMSWVESVLYYTGFPSGTPTTALLSRTPQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LSTIAERWVQVADKLDRDLFLRMTFSVINDT-----NGGKTVRAIFP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
              STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BURLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna Pieternella
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Pred. No. 4.8e-16;
5; Mismatches 198; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TINGSGPNQR- 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10023 - 7604
ZIP: 10023 - 7604
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy dis:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-SEP-1 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LAGENEG,
APPLICANT: PONSTEIN,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP96
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 04-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 25-FEE CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK
STATE: NY
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                                                                                                                                                                                                                                                                                                            179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TPD--NSSFPSVLOAYIR-----NLRFNEST-TPKPILITALHPSHIQAAVVCAK-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 TPDKPDPRLPSMKQGFNRRWIGTNIDFVYVVYTPQG--ACTALD----RAMEKCSPGTVR
                                                                                                                                                                                                                                                                                                                                                   EVYYRIAEKSNSHAFPAGVCPTVGVGGHFSGGGYGNLMGKYGLSVDNIVDAQLI-----
                                                                                                                                                                                                                                                                                                                                                                                     WGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLT 178
                                                                          GSGPNQRGKYKSAYMIKDFPDFQIDV-----IW----KYLTEVPDGL-TSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                             LLMKTRSGGHDYEGLSYVTNSNQPFFVVDMFNLRSINVS-----IEDETAWVQAGATLG 160
                                                                                                                                                     HLEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETIN
                                                                                                                                                                                                                              FTRDALODLLTKYFKLARCDWKNTVGKFOIFHQAAEEFVMYLYTSYSNDAEREVAQDRHY
                                                                                                                                                                                           --RTSEQNLSTIAHR-----W----IQVADKLDNDLFLRMTFNVINNTNGE-----
                                                                                                                                                                                                                                                                                                        EDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDG
                                                                                                                                                                                                                                                                      -DVNGKLLNRKSMGED--LFWAITGGGGVSFGVVVAYKIK-LVRVPTTVTVFNVQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 amino acids
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26 WEST 61 STREET
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VENTION: ANTIFUNGAL PROTEINS, DNA CODING
VENTION: THEREFOR, AND HOSTS INCORPORATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 266; DB 9;
23.5%; Pred. No. 1.7e-15;
ative 72; Mismatches 187
                                                                                                                 ----KTIRG----LFP-----
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                                      -KDFPELGVEISDCIEMSWIESVLFYTNFPIGTPTTALLSRTPQR
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  EMKDALLQVDMFGGEIHKVVWDATAVAQRE-Y 430
                                                                                                                   -TLYLGNST----ALVALLN
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US-09-258-031B-71
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                                                                                                                                                        US-09-258-031B-71
                                                                                                                                                                                                                                                                        APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/04923
FILING DATE: 04-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP97200831.2
PTITING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/09258031B Patent No. US20020168735A1
                                                                                                  Matches 118;
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION APPLICANT: STUIVE
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: I
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APPLICANT:
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APPLICANT:
                                                                                                                                                                    TOPOLOGY: 15 MOLECULE TYPE:
                                                                                                                                                                                                                                                               FILING DATE: 19-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: WINDOWN REFORM
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                              LENGTH:
116 DTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKP 175
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                                           MKIRSGGHDYDGLSYVTYSGKPFFVLDMFNLRSVDVDVASKTAWVQTGAILGEVYYYI--
                                                                     VRIVSGGHCYED----
                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                               508 amino acids
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MELCHERS, Leo Sjoerd
VAN DE ENTER-TROOST, Johanna Pieternella
                                                                                                  Conservative
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                                                                                                                                                                    protein
                                                                                                                                                                                                                                                       04-SEP-1996
                                                                                                               8.8%;
23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jerome Humbertina Henricus Victor
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                                                                                                                                                                                                                                                                    EP96202466.7
                                                                                                  67;
                                                                                                               Score 263; DB 9
Pred. No. 3e-15;
                                                                       ---FVFDECVKAIINV-----TGLVESGYDDDRGYFVSSG 115
                                                                                                  Mismatches
                                                                                                                           DB 9;
                                                                                                  201;
                                                                                                                             Length 508;
                                                                                                 Indels 122;
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               RESULT 10
US-09-880-748-1466
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  Sequence 1466, Application US/09880748
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US-09-932-923-1
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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Patent No. US20020064577A1
                                                                                        Matches
                                                                                                                   Query Match
Best Local :
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APPLICANT: POULSEN, CHARLOTTE H.
APPLICANT: HOSTRUP, PERNILLE B.
TITLE OF INVENTION: A METHOD OF IMPROVING THE PROPERTIES OF A FLOUR DOUGH,
TITLE OF INVENTION: A FLOUR DOUGH IMPROVING COMPOSITION AND IMPROVED FOOD
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: 59191-0000003
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/483,870
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/DK96/00239
PRIOR FILING DATE: 1996-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/932,923
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/676,186
PRIOR FILING DATE: 1996-07-12
                                                                                                                                                                                                                                       ORGANISM: Chondrus Crispus FEATURE:
                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ----DVNGKILDRKLMGED--LYWAINGGGGGSYGVVLAYKI-NLVEVPENVTVFRISRT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 KDALLQVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEM
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                                                                                          l Similarity
19; Conserv
                              DPGYIVIDVNAGTPDKPDP 26
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DPGYIVIDVNAGTPDKPDP 19
                                                                                             Conservative
                                                                                                              3.6%;
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                                                                                          0;
                                                                                          Score 107; DB; Pred. No. 0.0
                                                                                                                   DB 10;
                                                                                                                                                                                                                peptide
                                                                                                                                       Length 19;
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1466
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-124-880-4
                                                             PRIOR APPLICATION NUMBER: 60/084,358
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FREESEQ for Windows Versior
SEQ ID NO 4
LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10124880 Publication No. US20030026810A1
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                           APPLICANT: Andersen, Lene No. US20030026810Alboe
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. US20030026810Alel Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
CURRENT APPLICATION NUMBER: US/10/124,880
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US/9/311,626B
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US/08/98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jorgensen, Per Lina
APPLICANT: Schnorr, Kirk
       LENGTH: 622
TYPE: PRT
ORGANISM: Bacillus licheniformis
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                                                                                                                                                                                                            FILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLVTVSSGGGGSGGGG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GYDILTGYYMGSAFDQWGR-----
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                                                                                                                 for Windows Version
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                                                      APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727
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, Sequence 12135, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 FVSWRLLGTEPSSVSLNVYRNGKKLNGSPITSSTNYQDAGGDLN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSCYSVGLGGHIVGGGD-----GILARLH-GLPVDWLSGVEVVVKPVLTEDSVLKYV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKKG-KKRWKNLLAASSLLLITLVTGFSEQAEADGRTAAQARQMESLNRGLVAVKTGNGV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGNGAYAGQGNHSLSVADVDGDGKDEIIYGAMAV---DHDGKGLYSTGWGHGDAMHTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDPSRPGLEVFQVHENSNSPYGLSFRDAKTGKIIWGVHAGKDVGRGM---AADIDPRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VADWGDSYGNRVDRFLAGVAYLDGERPSFVMARGYYTRTVLVAYNFRGGKLTKLWTFDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KTADGTKDGKGKVIGNANADYRNAQGRILSGPEYLTVFKGDTGAELTTVNYEPARGN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FYALTETINGSGPN---QRGKYKSAYMIK-DFPDFQIDVIWKYLTE
                                                                                                                                                                                                                                                                                                                                            Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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20.4%; Pred. No. 5.9;
cive 81; Mismatches 212;
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5.9;
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352 391 349 235 246

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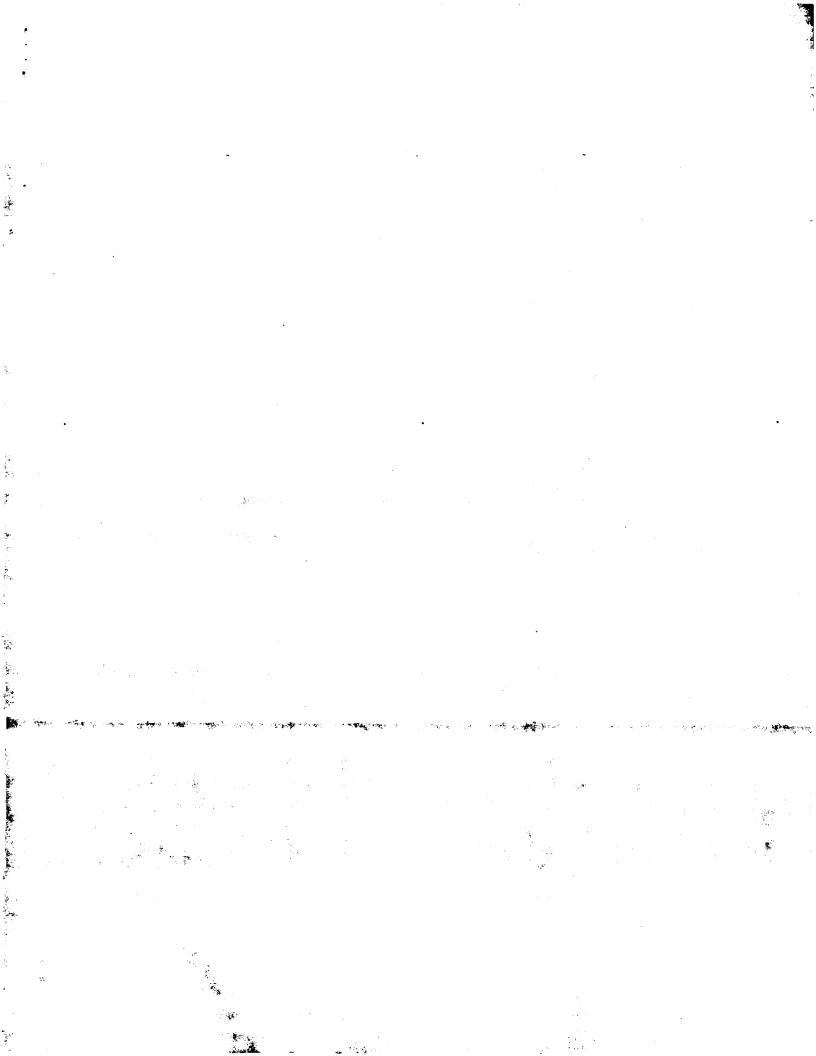
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; TYPE: PRT ; ORGANISM: Brassica US-10-234-026-13
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US-09-815-242-12135
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12135
LENGTH: 657
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10234026 Publication No. US20030097679A1 GENERAL INFORMATION:
                                                                                           SOFTWARE: FastSEQ for
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                     PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 09/423,468
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                   APPLICANT: Jens Ostergaard
APPLICANT: Marc Charles Ernest Van Montagu
TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
FILE REFERENCE: DECLES.001C1
CURRENT APPLICATION NUMBER: US/10/234,026
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: NL 1006000
PRIOR APPLICATION NUMBER: NL 1006000
PRIOR APPLICATION NUMBER: PCT/EP98/02830
PRIOR APPLICATION NUMBER: PCT/EP98/02830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 RYYLMRELPFGSDGVFTPEAFVERTNFDLAN-DLGNLVNRTISMINKYFDGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 EIVRFHSIIWPILLMALDLPLPKKVFAHGWILMKDGKMSKSKGNVVDPNILIDRYGLDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 VE---LVKEESYFFNISKYTDRLLEFYDQNPDFIQPPSRKNEMINNFIKPGLADLAVSRT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 YKSAYMIKDFPDF-----QIDVIWKYLTEVPDGLTSAEMKDALLQ------VDM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 RLLKQGDIYLGEYEGWYSVP-----DETYYTESQLVD-PQYENGKIIGGKSPDSGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TC--EPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETINGSGPNQRGK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 --KFQIFHQAA------EEFV----MYLYTSYSNDAEREVAQDRHYHLEADIEQIYK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 FGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 GOKIOEKAOKAGKTEIEYLDEMIAGIKOLWAKLEISNDDFIRTTEERHKHV----VEOVFE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 FYITTPIYY-----PSG----NLHIGHAYST--VAGDVIARYKRMQGYDVRYLTGTDEH
                                                                      600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFNWGVHVPSNPKHVVYVWIDALV---NYISALGYLS----DDESLFNKYWPADIHLMAK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guy Jerome Corneel Bauw
Mark William Davey
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                         oleracea
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19.1%; Pred. No. 6.4;
vative 51; Mismatches 139; Indels 144;
                                                                                                                         Windows Version 4.0
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; ORGANISM: Staphylococcus aureus
US-09-815-242-13013
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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Best Local Similarity
Matches 75; Conserv
                                                                                SOFTWARE: FastSEQ
SEQ ID NO 13013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13013, Application US/09815242 Patent No. US20020061569A1
                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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                                           LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 DVIWKYLTE-----VPDG------LTSAEMKDALLQVDMFG----GEIHKVVWDATAVA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 WAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQI 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 LGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELFWAHT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGLGG-LGVVAEV---TLQCVERQELLEHTYVS-----TLEEIKKNHKKLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDPNEI---FTNKQSIPTKP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESIVKYRVQDSSKKTPDSREPDINELSFTELRDKLIALDPLNDVHVGKVNQ-----A
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick, John D.
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                                                                                                           for Windows Version
                                                                                                                                  2001-02-16
)S: 14110
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17.9%; Pred. No.
tive 55; Mismatc
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ed. No. 6.9;
Mismatches 128; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Essential Genes
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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Vers
; SEQ ID NO 5013
; LENGTH: 584
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-5013
                                                                                                                                                                                         TITLE OF INVENTION: INSERTION: TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION UNMBER: US/9/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-26
PRIOR PRILING DATE: 2001-12-27
PRIOR PRILING DATE: 2001-12-27
PRIOR PRILING DATE: 2001-12-27
PRIOR PRILING DATE: 2001-12-16
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PRIOR PILING DATE: 2001-12-16
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US-09-815-242-5013
; Sequence 5013, Application US/09815242
; Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L
APPLICANT: Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 VE---LVKEESYFFNISKYTDRLLEFYDQNPDFIQPPSRKNEMINNFIKPGLADLAVSRT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 RLLKQGDIYLGEYEGWYSVP------DETYYTESQLVD-PQYENGKIIGGKSPDSGHE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 FGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVG----
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Zyskind, Judith W.
Wall, Daniel
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Yamamoto, Robert T.
Xu, H. Howard
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492 H 492
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                                                                                                                      -YEEMYEPYGGVPDPNTQVES-----GKGVFEGCYFNYPDVDLNNWKNGKYGALEL 506
                                                                                                                                                                     IL----MFGADKPEIVAAALGAV---
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Search completed: June 10, 2003, 10:07:16 Job time : 27 secs



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Result
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Listing first 45 summaries
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2997
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1: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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                                            US-08-652-877-84

US-09-255-829-22

US-09-255-829-29

US-09-255-829-20

US-08-790-912-4

US-09-134-001C-5226

US-09-609-134-01C-5226

US-08-669-304-2

US-08-669-304-9
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US-09-36-987A-11

US-09-370-700-11

US-09-433-248A-2

US-09-433-248A-6

US-09-647-390-16

US-09-647-390-18

US-09-647-390-18

US-09-647-390-18

US-09-647-390-18

US-09-217-490-2

US-09-433-248A-8

US-09-433-248A-8

US-09-411-626B-4

US-09-311-626B-4

US-09-423-468A-13

US-09-423-468A-13

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US-08-652-877-12
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Sequence 6, Appli
Sequence 16, Appl
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Sequence 17, App
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Sequence 11, Appl
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US-08-448-489-13 US-08-448-464A-20 US-08-415-136-20 US-08-957-310-20 US-08-957-310-21 US-08-957-310-21 US-08-957-310-21 US-08-957-310-21 US-08-957-310-21 US-08-957-310-21 US-08-957-310-21 US-08-955-336-30 US-08-480-604A-30 US-08-480-604A-10 US-08-955-336-10 US-08-955-336-10 US-08-957-310-10

ALIGNMENTS

#### RESULT 1 US-08-669-304-31 US-08-669-304-31 COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/669,304 FILING DATE: 12 July 1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UNMBER: 08/476,910 FILING DATE: 7 June 1995 ATTORNEY/AGENT INFORMATION: NAME: Stanislaus Aksman NAME: Stanislaus Aksman Sequence 31, Appr. Sequence 31, TELEX: NO. 6251626e INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM FC compatible COMPUTER: TOO MG. APPLICANT: Peter Stougger APPLICANT: Ole Cai Hansen TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, TITLE OF INVENTION: METHOD OF PRODUCING SAME AN SEQUENCE CHARACTERISTICS: LENGTH: 546 amino acids TYPE: amino acid TOPOLOGY: linear REFERENCE/DOCKET NUMBER: 32 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 955-1926 CORRESPONDENCE ADDRESS: MOLECULE TYPE: protein COUNTRY: U.S.A. ZIP: 20006-1109 STATE: D.C CITY: Washington TELEFAX: REGISTRATION NUMBER: ADDRESSEE: Hunton & Williams STREET: 1900 K Street, N.W. Application US/08669304 (202) 778-2201 28,562 320.000003 PRODUCING SAME AND USE OF SUCH ENZYME

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1 MATLPQKDPGYIVIDVNAGTPDKPDPRLPSMKQGFNRRWIGTNIDFVYVVYTPQGACTAL 60

Matches 545; Query Match Best Local Similarity

Conservative

0,

Score 2989; DB 4; Pred. No. 3.1e-296; 0; Mismatches 1;

Length 546; Indels

0;

Gaps

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99.7**%**; 99.8**%**;

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
            SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
                                                                                                                                                APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic
TITLE OF INVENTION: Production
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                               COUNTRY:
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Merlo, Donald J.
Treadway, Patti J.
Turner, Jan R.
                                                                                                                                                                                        9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                            Baltz, Richard H.
Broughton, Mary C.
Crawford, Kathryn P.
Madduri, Krishnamurthy
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Ge
FILE REFERENCE: 50489 DIV1
                                                                                                                      Sequence 11, Application US/09370700 Patent No. 6274350 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 539 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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TYPE: amino acid
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               Genes
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                  For
                  Spinosyn Insecticide
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508 502

450 394 390 350 330 302 284 254

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121 SFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTED
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                                                                        LGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLKEPKQ 544
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KDNYPRLQRAKARWDPQNIFQHGLSIKPPARLSPGQ 538
                                                                                                                                                         TWIRGFYREMYAETGGVPVPGTRV-----DGSYINYPDTDLADPLWNTSGVAWHDLYY
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GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Fancou, Omolayo O.
APPLICANT: Han, Feng
APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Disease Resistance Factors
FILE REFERENCE: BB1252 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60,107,242
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 8
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US-09-433-248A-2
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; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-11
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Best Local Similarity
Matches 174; Conserv
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CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                        Sequence 2, Application US/09433248A Patent No. 6355462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTED
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                                                                                                                                                                                                                                                                                                                                                                                KDNYPRLQRAKARWDPQNIFQHGLSIKPPARLSPGQ 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNN--WKNGKYGALELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKRHTSKTSYMHDETMDYPFYALTETINGSGPNORGKYKSAYMIKDFPDFQIDVIWKYLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIVE-ADRNSTGAGHDLWWAHTGGGGGNFGIVTRFWLRTPDVVSTDAAELLPRPPATVLL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVR--TGRRVGVRSGGHCFENLVADPAIRVLVDLSELNRVYYDSTRGAFAIEAGAALGQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                           LGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLKEPKQ 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPVRP 330
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                                                     Query Match
Best Local Simi
Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: Microsoft Office
SEQ ID NO 2
LENGTH: 397
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                              SOFTWARE: Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09433248A Patent No. 6355462 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/433,248A CURRENT FILING DATE: 1999-11-04 PRIOR APPLICATION NUMBER: 60/107,242 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                     APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
TILE OF INVENTION: Disease Resistance
FILE REFERENCE: BB1252 US NA
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Falco, S. APPLICANT: Famodu,
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                            ORGANISM: Glycine
                                                                                                                                                               TYPE: PRT
                                                                                                                                                                               LENGTH: 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 DSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQDLL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
36 NRRWIGTNIDFVYVVYTP-----QGACTALDRAMEKCSPG---TVRIVSGGHCYEDFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 RVLAFPAGICPTVGVGGHLSGGGFGTLMRRYGLAAD-----NVIDAVLV-DADGRLLNR
                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTMGED--LFWAIRGGGGESFGVVLSWKLR-LVRVPETVTVFTVRRS----INQSASHLI 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFPHRKGNLYNLQYYSYWFENGTAALEKRMSWVRGLYEEM-EPYVS-KNPRTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVAQRE-YIIKLQYQTYWQEEDKDAV--NLKWIRDFYEEWYEPYGGVPDPNTQVESGKGV
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                                                       Conservative
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                                                   10.1%; Score 304; DB 4; 23.6%; Pred. No. 3.4e-22; ative 77; Mismatches 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395
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                                                     Mismatches 205;
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                                                                                     Length 529;
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                                                     Indels 136; Gaps
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APPLICANT: Custers, Jerome
APPLICANT: Simons, Lambertus
TITLE OF INVENTION: Pathogen-Inducible Promoter
FILE REFERENCE: MOG 57707/UST
CURRENT APPLICATION UNMEER: US/09/647,390
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: EP 98201024.1
PRIOR APPLICATION UMBER: EP 98201024.1
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                    ; LENGTH: 538
; TYPE: PRT
; ORGANISM: Helianthus
US-09-647-390-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No. 6465636; GENERAL INFORMATION:
; APPLICANT: Stuiver;
; APPLICANT: Custers,
; APPLICANT: Simons,
                                                                                                                                        Query Match
Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                 SOFTWARE: 1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09647390 Patent No. 6465636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 VVWDATAVAQRE-YIIKLQYQTYWQEEDKDAV--NLKWIRDFYEEMYEPYGGVPDPNTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 LSDVPFVMVDLINIRS-IEINLADETAWVQAGASIGELYYKISKA-SKVHG--FPAGTCP 172
                      83
                                                           43
TALDRAMEKCSPGTVRIVSGGHCYED----
                                                           DRADPSFPITGEVYTPGNSSFPTVLONYIRNLRFNETTTPKPFLIITAEHVSHIQAAVVC
                                                                                                   DKPDP-----
                                                                                                                                                                                                                                                                                                                        PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESGKGVFEGCYFNYPDVDL---NNWKNGKYGALEL----YFLGNLNRLIKAKWLWDPNEIF
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                                                                                                                                          Conservative
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                                                                                                                                                           9.2%;
                                                                                                                                      ; Score 275; DB 4; Length 538; 
; Pred. No. 3.1e-19; 
64; Mismatches 197; Indels 1
                                                                                               -RLPSMKQGF--NRRWIGTNIDFVYVVYTPQG-----AC
-----FVFDECVKAIINV----TGLVE 101
                                                                                                                                      197; Indels 198;
                                                                                                                                        Gaps
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                                                                                                                                          26;
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APPLICANT: Simons, Lambertus
TITLE OF INVENTION: Pathogen-Inducible Pron
FILE REFERENCE: MOG 57707/UST
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: EP 98201024.1
PRIOR APPLICATION NUMBER: EP 98201024.1
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 540
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                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                           ORGANISM: Lactuca sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 RVPEVVTV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 SVDNIVDAQII------DVNGKLLDRKSMGED--LFWAITGGGGVSFGVVLAYKIK-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 SGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGL
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                                                                                                                                          140;
                                                           56 TPD--NSSFPSVLQAYIR-----NLRFNEST-TPKPILITTALHPSHIQAAVVCAK-THR
74 IV----SGGHCYED-----
                                                                                                   20 TPDKPDPRLPSMKQGFNRRWIGTNIDFVYVVYTPQG--ACTALD----RAMEKCSPGTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AFLNYRDLDIGINSHGRNAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFFRNEOS
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON: Pathogen-Inducible Promoter MOG 57707/UST
                                                                                                                                        8.9%; Score 266; DB 4; I
23.5%; Pred. No. 2.6e-18;
ative 72; Mismatches 187;
---FVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTN 118
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                                                                                                                                                                             Length 540;
                                                                                                                                          Indels 198;
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RESULT 8
US-09-217-490-2
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CURRENT APPLICATION NUMBER: US/09/217,490
CURRENT FILING DATE: 1998-12-21
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: PA 1998 00763
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-12-23
                                                                                                                                                                           SEQ ID NO 2
LENGTH: 495
TYPE: PRT
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                                                           Matches
                                                                               Query Match
Best Local :
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                                                                                                                                        ORGANISM: Microdochium nivale
-09-217-490-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fuglsang, Claus Crone
APPLICANT: Xu, Feng
APPLICANT: Solightly, Elizabeth
TITLE OF INVENTION: Carbohydrate Oxidase And
TITLE OF INVENTION: Baking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schneider, Palle
APPLICANT: Christensen, Soren
APPLICANT: Dybdal, Lone
                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Ve
                                                                               Local Similarity
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76 SGGHCYEDFVF-DECVKAIINVTGLVE-SGYDDDRGYFVSSGDTNWGSFKTLFRD-HGRV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNPFKIKSDYVKNTISKQGFESIFERMKELENQMLAFNPYGGRMSEISEFAKPFPHRSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAKIQYEVNWDELGVEAANRYLNFTRVMYDYMTPFVSKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIKLQYQTYWQEEDKDAVN--LKWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNY 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDSVLKYVHKDSEGNDGELFWAHTGGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DVNGKLLNRKSMGED--LFWAITGGGGVSFGVVVAYKIK-LVRVPTTVTVFNVQ-----
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                                                             Conservative
                                                                             8.5%; Score 255; DB 4; Length 495; 24.2%; Pred. No. 3e-17;
                                                                                                                                                                                                                                       Windows Version
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                                                       77;
                                                           Mismatches 175; Indels 126;
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                                                           27;
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Disease Resistance Factors
FILE REFERENCE: BB1252 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,242
PRIOR FILING DATE: 1998-11-05
INUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 129
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                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 40
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Triticum aestivum
                                  512 LNRLIKAKWLWDPNEIFTNKQSIP
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  104 YQRLASVKAAVDPMDYFRNEQSIP 127
                                                                                                                  462 EPYGGVPDPNTQVESGKGVFEGCYFNYPDVDL-----
                                                                                                                                                                                            405 LLQVDMFGGEIHKVVWDATAVAQRE---YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 FGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 LTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDA--LLQVDM 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 --VTLNWKNKTSALKGI-EAVEDYARWV-----APREV----NFRIGDYGAGNPGIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
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                                                                                                                                                         1 LIVLEPHGGLMATIPTAATPYPHRSGVLYII--QYIAFWQGDGGTAAT-TWLGSFYDFMG
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                                                                               HYVSSNP-
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                                                                                                                                                                                                                              3.9%; Score 117; DB 4; 27.8%; Pred. No. 0.00042; cive 17; Mismatches 57;
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                                                                           --RQAYVNFRDLDIGQNAVSDDLSTTSQSGKVWG-ERYFMSN 103
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US-08-676-186-1
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                                                                                                                                                                                                                                          RESULT 11
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GENERAL INFORMATION:
APPLICANT: SOE, J
                                                                                                                                                      Sequence 4, Application US/09311626B Patent No. 6399347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                APPLICANT: Andersen, Lene No. 6399347boe
APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
TITLE OF INVENTION: NO. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
                                                                                              APPLICANT: Jorgensen, Per
APPLICANT: Schnorr, Kirk
APPLICANT: Andersen, Lene
CURRENT APPLICATION NUMBER: US/09/311,626B
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,186
FILING DATE: 12-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20006-2296
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Akaman, Stanislaus
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 44648/013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANI: OF INVENTION: A method of improving the TITLE OF INVENTION: A method of improving the properties of a flour dough, a flour dough improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                         DPGYIVIDVNAGTPDKPDP 19
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COUNTRY: USA
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TELEFAX: 202-778-8335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 107; DB 4;
100.0%; Pred. No. 0.0002;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                       RESULT 12
US-09-423-468A-13
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 622
GENERAL INFORMATION:
APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
APPLICANT: Guy Jerome Corneel Bauw
APPLICANT: Mark William Davey
APPLICANT: Mark William Davey
APPLICANT: Jens Ostergaard
APPLICANT: Marc Charles Ernest Van Montagu
TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
FILE REFERENCE: DECLES.001AC
CURRENT APPLICATION NUMBER: US/09/423,468A
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                         Sequence 13, Application US/09423468A Patent No. 6469149
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 0600
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-05-05
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                                                                                                                                                                                                                                                                                                                                                                 467 AEVWANGSLYTAKGVKIGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 APGNGAYAGQGNHSLSVADVDGDGKDEIIYGAMAV---DHDGKGLYSTGWGHGDAMHTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 HKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 MKQGFNRRW----IGTNIDFVYVV--YTPQ----GACTALDRAMEKCSPGTVRIVSGGHC
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Pred. No. 0.94;
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PRIOR APPLICATION NUMBER: NL 1006000

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Query Match
Best Local Similarity
Thes 75; Conserve
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US-08-704-711A-17
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows
SEQ ID NO 13
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08704711A Patent No. 6114159
GENERAL INFORMATION:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILLING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WILL, HOTSE
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                  CITY: Washington
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 VGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 IGGIIQVGAHGTGARLP--PID----EQVIGMKLVTPAKGTIELSKD---NDPELFHLAR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 LGGHIVGGGDGILARLHGLÞVDWLSGVEVVVKÞVLTEDSVLKYVHKDSEGNDGELFWAHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QREYIIKLQ-YQTYWQEE--DKDAVNLKWIRDFYEEMYEFYGGVPDPNTQVESGKGVFEG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESIVKYRVQDSSKKTPDSREPDINELSFTELRDKLIALDPLNDVHVGKVNQ-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGLGG-LGVVAEV---TLQCVERQELLEHTYVS-----TLEEIKKNHKKLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAEFWKKSEGYRVGWSDEILGFDCGGQQWV----SETCFPAGTLAKPSMK------
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DE 4438838.1
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                                                                                                                                                                     Version #1.30
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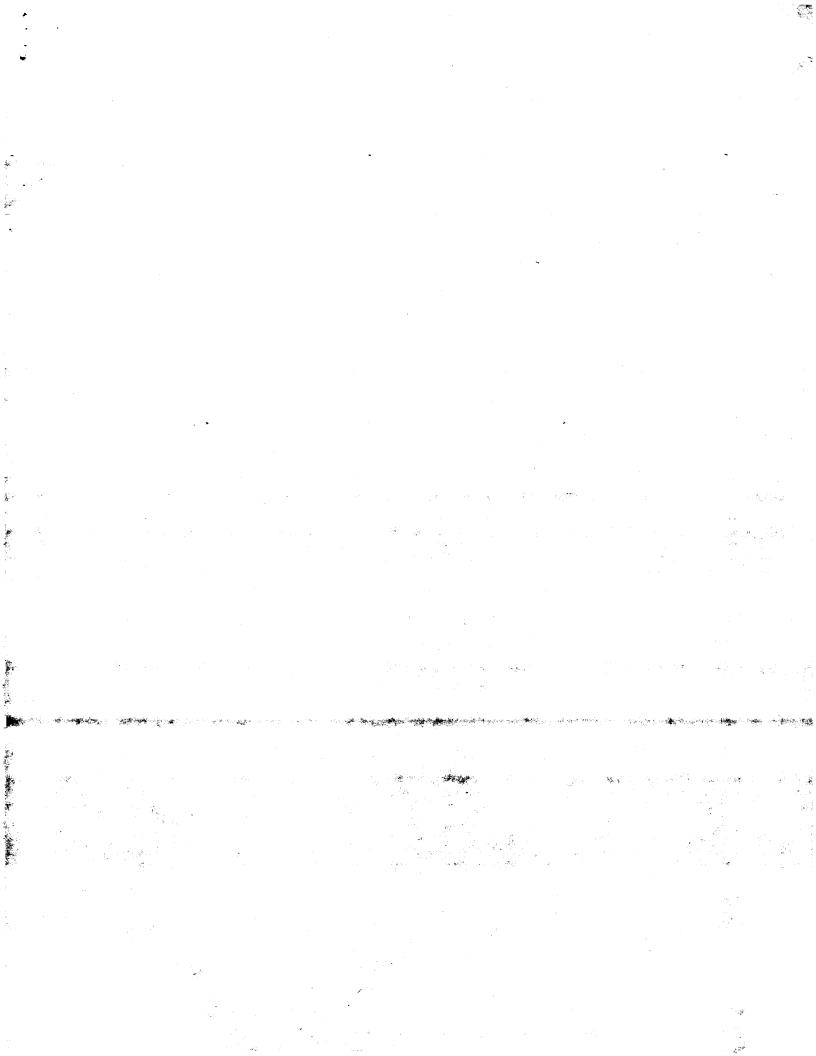
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RESULT 14
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 440
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: GRANADOS, PATRÍCIA D.
REGISTATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
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                        TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
                  NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                         APPLICANT: WILL, Horst
                                                                                                                                                                                                                                                                                          494
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                                                                                                                                                                                                                                                        453 RVARGNKWLNCRYG 466
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                                                                                                                                                                                                                                                                                                                             RYDNQRQFMEPGYPKSISGAFFG----IESKDAVFQQEHFFHVFSGPRYYAFDLIAQRVT 452
                                                                                                                                                                                                                                                                                                                                                                 IRDFYEEMYEP-----YGGVPDPNTQVESGKGVFEGCYF-----NYPDVDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGPNQRGK---YKSAYMIKDFPDFQ-----IDVIWKYLTEVPDGLTSA-EMKDALLQV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AEETWTNTSANYNLFLVAAHEFGHSLGLAHSSDPGALMYPNYAFRETS---NYSLPQ
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                                                                                                                                                                                                                                                                                          ----NNWKNGKYG 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDIDGIQAIY-----GLSSNPIQPTGPSTPKPC---DPSL--TFDAIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HTGGGGGNFGIITKYYFKD----LPM-SPRGVIASNLHFSWDGFTRDALQDLLTKY 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TLRGEILFFKDRYFWRRHPQLQRVEMNFISLFWPSL---PTGIQAAYEDFDRDL-I
ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 92; DB 3; 20.2%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE 4409663.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KDAFELWSVA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 158; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 20.2 les 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
PILING DATE: <Unknown).
APPLICATION NUMBER: DE 4438838.1
PILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
PILING DATE: 17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                        342
                                                                                409
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                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                            252
453
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                                                                                                                                                                                                                                            303 D----IEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETIN 358
                                                                                                                                                                                                                                                                                                                                                                    144 SPLIFTRISQGEADINIAFYQRDHGDNSPFDGPNGILAHAFQ-PGQGIGGDAHFD-----
                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 LGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELFWA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 INVTGLVES-----GYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVG 142
IRDFYEEMYEP-----YGGVPDPNTQVESGKGVFEGCYF-----NYPDVDL-----
                                                                                DMFGGEIHKVV--WD--
                                                                                                                                                              GSGPNQRGK---YKSAYMIKDFPDFQ-----IDVIWKYLTEVPDGLTSA-EMKDALLQV 408
                                                                                                                                                                                                                                                                                                                            FKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSND-----AEREVAQDRHYHLEA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNVTGKPNEETLDMMKKPRCGVPDSGGFMLTPGNPKWERTNLTYRIRN-------
                                     FLFKGNQYWALSGYDILQGYPKDISNYGFPSSVQAIDAAVFYRSKTYFFVNDQ-----FW
                                                                                                                                                                                                      DDIDGIQAIY-----
                                                                                                                                                                                                                                                                                                                                                                                                          ----HTGGGGGNFGIITKYYFKD----LPM-SPRGVIASNLHFSWDGFTRDALQDLLTKY 251
                                                                                                                                                                                                                                                                                      ---AEETWINTSANYNLFLVAAHEFGHSLGLAHSSDPGALMYPNYAFRETS---NYSLPQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 466 amino acids
TYPE: amino acid
STRANDEDNESS: single
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21-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/521,220 FILING DATE: 08-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                        ----TLRGEILFFKDRYFWRRHPQLQRVEMNFISLFWPSL---PTGIQAAYEDFDRDL-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------YTPQLSEAEVERAI-----KDAFELWSVA 143
                                                                                                                                                                                                      -GLSSNPIQPTGPSTPKPC---DPSL--TFDAIT----
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                                                                           -ATAVAQREYIIKLQYQTYWQEEDKDAVNLKW 452
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                                                                                                   Matches
                                                                                                                              Query Match
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                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein,
TITLE OF INVENTION: Thereof and DNA Encoding Same
                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word 6.0 (P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1.
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                                                                                                                                                                                                               LENGTH: 944 amino acids
                                                                                                                Local
                                                                                                                                                                                                                                                                                                              NAME: Savitzky, Martin
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
SOFTWARE: Word 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 RYDNQRQEMEPGYPKSISGAFPG----IESKDAVFQQEHFFHVFSGPRYYAFDLIAQRVT 452
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371 AYMIKDFPDF------QIDVIWKYLTEVPDGLTS----
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                                                                                                                Similarity
                                                                                                                                                                                                  amino acid
                                         PDNVRIRKYNLSSERFSEYLQDEEYIQAVDYDWDPKDIGLSVVYYTVRGEG-SRFGAIKR
                                                                     PFPVRPRKRHTSK---TSYMHDE----TMDYPF-----YALTETINGSGPNQRGKYKS
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500 Arcola Rd., 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crumley, Gregg w. Morse, Clarence C.
                                                                                                                                                                                                                                                             610-454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murray, Edward M.
Hjalm, Goran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Juhlin, Claes
                                                                                                   Conservative
                                                                                                                                                                                                                                                                          610-454-3816
                                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-1994
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                                                                                                                3.1%;
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0 (Patentin)
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                                                                                                                                                                                                                                                                                                                   29,699
                                                                                                                                                                                                                                              12:
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                                                                                                                                                                                                                                                                                                       A1355E-US
                                                                                                                Score 92;
Pred. No.
                                                                                                   Mismatches
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                                                                                                                               DB 4;
                                                                                                   90;
                                                                                                                              Length 944;
                                                                                                    Indels
                 ----AEMKDALLQVDMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragments
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                 412
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Qy Db Search Job tim	B 4	운 명
QY 467 VPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDP 524  Db 507 -EDRNILVFEDLGWPTGLSIDYLNNDRIYWSDFKEDVIETIKYDGTDRRVIAKEAMNP 563  Search completed: June 10, 2003, 10:00:51  Job time : 20 secs	462 GRYRKWIISTDLDQPAAIAVNPKLGLMFWTDWGKEPKIESAWMNG 506	407 AYIPNFESGRNNLVQEVDLKLKYVMQ-PDGIAVDWVGRHIYWSDVKNKRIEVAKLD 461



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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                       SPTREMBL 21:*

SPTREMBL 21:*

Sp archea:*

Sp bacteria

Sp fungi:*

Sp invert

Sp invert

Sp mamma

Sp mamma

Sp morga

Sp pha

Sp pha

Sp pha

10: Sp r

12: Sp r

13: Sp r

14: SF

15: SF

16: '
                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
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Gapop 10.0 , Gapext 0.5
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2997
1 MATIPQKDPGYIVIDVNAGT.....IFTNKQSIPTKPLKEPKQTK 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June 10, 2003, 09:54:36; Search time 35 Seconds (without alignments) 3214.335 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                           sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                         sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_virus:*
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sp_mammal:*
                                                                                                                                                                                                        sp_plant:*
SUMMARIES
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
249.5	5	252	266	272	272.5	272.5	273	274	274	275.5	277	277.5	278	278.5	294.5	296	297	298.5	300	300.5	301	302.5	8	304.5	305	317.5	322	324.5
8.3	8.4	8.4	8.9	•					9.1										10.0		10.0		10.1		10.2	10.6	10.7	10.8
540	464	531	540	538	530	530	535	536	532	715	527	526	533	447	541	536	533	527	532	532	542	552	537	552	542	534	540	541
10	N	10	10	10	10	10	10	10	10	10	10	10	10	16	10	10	10	10	10	10	10	10	10	10	10	10	10	10
064745	Q9КНК2	Q9SA86	Q8SA60	Q8SA59	Q9SUC6	Q94 KD7	Q9FI25	Q9ZPP5	Q9FKV2	Q9LNL9	Q9SA85	Q9SA88	Q9SA89	006997	Q9FKV0	Q9SA99	Q9FI21	Q9FZC6	Q9SVG5	064743	Q93Y11	Q9FZC7	Q9FKU8	Q8RWA4	Q9FKU9	Q93ZA3	Q9SVG4	Q9LPC3
S	Q9khk2 s	Q9sa86	Q8sa60	Q8sa59	Q9suc6	Q94kd7	Q9fi25	2ddz6D	Q9fkv2	Q9lnl9	Q9sa85	Q9sa88	Q9sa89	006997	Q9fkv0	Q98a99	Q9fi21	Q9fzc6	Q9svg5	064743	Q93y11	Q9fzc7	Q9fku8	Q8rwa4	Q9fku9		Q98vg4	Q91pc3
arabidopsis	streptomyce	arabidopsis	lactuca sat	helianthus	arabidopsis	arabidopsis			arabidopsis	arabidopsis	arabidopsis	arabidopsis	arabidopsis	bacillus su	arabidopsis													

# ALIGNMENTS

Db	Ş	g 8	B 8	M B Q	AC DE DO	RESULT
121 SFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTED 180	121 SFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTED 180	61 DRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWG 120 	1 MATLPOKDPGYIVIDVNAGTEDKEDDRLESMKOGENRRWIGTNIDEVVVVYTPOGACTAL 60 	Query Match 100.0%; Score 2997; DB 10; Length 546; Best Local Similarity 100.0%; Pred. No. 1.1e-222; Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	p93762 PRELIMINARY; PRT; 546 AA.  p93762; 01-MAY-1997 (TrEMBLrel. 03, Created) 01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-UN-2002 (TrEMBLrel. 21, Last annotation update) 01-UN-2002 (TrEMBLrel. 21, Last annotation update) Hexose oxidase. Chondrus crispus (Carragheen). Elkaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinaceae; Chondrus. NCBI TaxID=2769; [1] SEQUENCE FROM N.A. MEDLINE=97269074; PubMed=9111074; Hansen O.C., Stougaard P.; "Havose oxidase from the red alga Chondrus crispus. Purification, molecular cloning, and expression in Pichia pastoris."; J. Biol. Chem. 272:11587-11587(1997). EMBL; U89770; AAB49376.1; EMBL; U89770; AAB49376.1; EMBL; U89770; AAB49376.1; EMBL; U89770; AAB49376.1; EMBL; U89770; FAD_binding 4; 1. EMBL; BEQUENCE 546 AA; 61899 MW; BDDEA46D53C870B1 CRC64;	IIT 1

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                                                                                                            Query Match
Best Local S
Matches 196
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Q8Y3D0;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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                                                                                                                                                                   Pfam; PF01565; FAD binding 4; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 508 AA; 56031 MW; BD8F025998BC3C84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein RSc0050. RSC0050 OR RS01873.
                                                                                                                                                                                                             EMBL; AL646057; CAD13578.1; -
InterPro; IPR001575; Oxid_FAD_
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Ralstonia
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RPTVR--SGGHCYEDFVSNNPGGVIVDLSLLNAPEVRADGAVRVPAGMQNWNGALELYKR
                         PGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKTLFRD 128
                                                                                IVIDVNAGTPDKPDPRLPSMKQGFNRRWIGTNIDF---VYVVYTPQGACTALDRAMEKCS
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                            Conservative
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                                                      -RQDPRYDTLRHGFNLRWPSSDAQAAGRIALCEKTDEVAPALQRIIDTGM
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35.2%;
                                                                                                           Score 771.5; DB 16; Length Pred. No. 4.2e-51; 4; Mismatches 202; Indels
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Query Match
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Matches 195;
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                   STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINB=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:533-527(2001).

BMBL; Ay414142; CAC89170.1; -.
                                                                                                                             Pfam;
                                                                      Hypothetical
                                                                                                                                          InterPro; IPR003610; CBM 5 12.
InterPro; IPR003961; FN III.
InterPro; IPR001575; Oxid PAD bind
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
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                                                                                                  PF02839; CBM 5 12; 1.
PF02839; CBM 5 12; 1.
PF01565; FAD_binding_4; 1.
                                                                                                PF01565; FAD 1
PF00041; fn3;
                                                     SM00060; FN3; 1.
etical protein; Complete proteome.
ICE 685 AA; 75266 MW; 597853869F657CC6 CRC64;
              Similarity
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24.6%; Silarity 33.6%; P. Conservative 77;
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Last annotation updat
Score 736.5; DB 1
Pred. No. 3.2e-48;
7; Mismatches 205
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                             DB 16;
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                             Length 685;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 16, Last annotation update)
Redenbach M., Kieser H.M., Denapalte U., Elling I., Redenbach M., Kieser H.M., Denapalte U., Elling I., Rinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                             STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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Cerdeno A.M., Parkhill J., I
Submitted (JAN-2001) to the
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STRAIN=A3(2);
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete St. coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL512902; CACC22143.1; -.
InterPro; IPR001575; Oxid FAD bind.
Pfam; PF01565; FAD binding 4; -1.
SEQUENCE 550 AA; 59895 MW; EB4A23E0F58E4ABC CRC64;
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01-DEC-2001
01-JUN-2002
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InterPro; IPR001575; Oxid FAD bind Pfam; PF01565; FAD binding 4; 1.
PROSITE; PS00862; Ox2 COVAL FAD; UI SEQUENCE 539 AA; 58473 MW; C4AI
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Chem. Biol. 8:487-499(2001).
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Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21257765; PubMed=11358695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=60894;
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FAD; UNKNOWN 1.
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Last sequence up
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Redenbach M., Kieser r....,
Rinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
"^1 Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harris D.E., Quall M.A., Kieser H., Collins M. Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model coelicor A3(2).";
Nature 417:141-147(2002).

EMBL; AL591083; CAC37882.1; -.
InterPro; IPR001575; Oxid FAD bind.
Pfam; PF01565; FAD binding 4; 1.
SEQUENCE 545 AA; 58522 MW; 4D72C37P
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STRAIN=A3(2) / M14
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                                                             QIYKTCEPTKALGGHAGWA-PFPVRPRKRHTSKTSYMHDETMDYPFYALT-ETINGSGPN
                                                                                                     SAWHVANASADHPYARLFSALKPRHRSAGEFLM--
                                                                                                                                           KL----ARCD--WKNTVGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDRHYHLEADIE
                                                                                                                                                                                     GAGGGNYGIVTRYWFRNDAGGLDPAALLPRAPRELIISEVTFPWDNTMTEAAFSRLLRNF
                                                                                                                                                                                                                      GGGGGNFGIITKYYFKD------LPMSPRGVIASNLHFSWDGFTRDALQDLLTKYF
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, Parkhill J., Ba
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e EMBL/GenBank/DDBJ databases.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4D72C37A5433B76A CRC64;
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                                                                                                       ·STQIDAAVPGADAL---
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QBVWA5
QBVWA5
QBVWA6
QBVWA6
QBVWAC
QBVW
AC QBVW
AC QBVW
DT 01-M
DT 01-M
DT 01-J
DE AC10
GN AC10
GN AC11
COC AC11
COC AC11
COC NCB1
RN [1]
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Matches 159;
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Q8VWA5;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AB008466; BAB72054.1; .
InterPro; IPR001875; Oxid FAD bind.
Pfam; PF01565; FAD binding 4; 1.
SEQUENCE 489 AA; 53652 MW; BA006ADAA0BA33E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces galilaeus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chung J., Fujii T., Tsukamoto N., Sankawa U., Ebizuka Y., "Aklavinone-aclacinomycin biosynthesis gene cluster from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=3AR-33;
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370
                           414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   DKPDPRLPSM-KQGFNRRWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGTVRIVSGGHC
                        EIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQ
                                                       ----DTGGFDRTKSKGAYLRKPWTAAQAATLYRHLS--ADSQVWGE-----VSLYSYGG
                                                                                                                                                                         IIDNHGAWHQRNSAAGTPYASMHSVFYLNSRAAGQILLDIQTDGGLDGAETLLND----F
                                                                                                                                                                                                       LLTKY-----FKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDRHYHL 300
                                                                                                                                                                                                                                                                FWAHTGGGGGGNFGIITKYYFKD-----LPMSPRGVIASNLHFSWDGFTRDALQD 246
                                                                                                                                                                                                                                                                                                                          SVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGND--GEL
                                                                                                                                                                                                                                                                                                                                                                                      YEDFVFDECVKAIINVTGLVESGYDD-DRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCY
                                                                                                                                                                                                                                                                                                                                                                                                                  DRADRRYQDLVTRGFNGRFRG-RPDVVYVVHTADQVVDAVNQAV--AAGRRIAVRSGGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGAFINYADADLADPALNTSGIGWNTLYFKDGYCRLQAAKTQWDPRNVFTHALGI 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATATAQRDSVIKMLFVNLMATEAEDRRNLAWVREFYRDVFAATGGVPRPS------GVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKGRFKAKSAYLRKTLPDAQIKAFYKHLTR-----TDYDNPAALVEIAGYGAAANLPASW
KVNSVPETATATAQRDSIIKVWMSATWMDPAHDDANLAWIREIYREIFATTGGVPVPDDR
                                                                                   TETINGSGPNORGKYKSAYMIKDFPDFOIDVIWKYLTEVPDGLTSAEMKDALLQVDMFGG
                                                                                                                 VAAVNEGTGVEPAVQRTTEP-----WL----RATLANKF-----
                                                                                                                                             EADIEQ-----IYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYAL
                                                                                                                                                                                                                                    WWAHTGGGGGNFGIVTRYWFRTPGATGTDPSALLPKAPTSTLRHIVTWDWSALTEEAFTR
                                                                                                                                                                                                                                                                                               QVGVGGHVLGGGYGPLSRRDGVVADHLYAVEVV---VVDASGQARKVVATSAADDPNREL
                                                                                                                                                                                                                                                                                                                                                          FEGFVDDPAVRAVIDMSQMRQVFYDSGKRAFAVEPGATLGETYRALYLDWGVTIPAGVCP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGCYFNYPDVDLNN--WKNGKYGALELYFLGNLNRLIKAKWLWDPNEIFTNKQSI 4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRGKY--KSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQVDMFGGEIHKVVWD
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 590.5; DB 2
29.3%; Pred. No. 3.6e-37;
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21,
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Best Local Similarity
Matches 135; Conserv
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Q9ZAR8;
Q1-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (Tremblrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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            421
                                        414
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                                     EIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDP 470
                                                                                                                               ---TRPDAEELTDRFIREVSRSVG-----ARPEVSVTT-----LPWLAAT
                                                                                                                                                           HYHLEADIEQIYKTC--EPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALT
                                                                                                                                                                                                                   DLLTKYFKLARCDWKNTVGKFQIFHQ-----AAEEFVMYLYTSYSNDAEREVAQDR
                                                                                                                                                                                                                                                                  HTGGGGGNFGIITKYYFKD-------LPMSPRGVIASNLHFSWDGFTRDALQ
                                                                                                                                                                                                                                                                                                            VGGHIAGGGGGALSRTYGLSVDHLHGVEVV---VVDSGGRARLVRATREPSDPHRDLWWA
                                                                                                                                                                                                                                                                                                                                 LGGHIVGGGDGILARLHGLPVDWLSGVEVVVVKPVLTEDSVLKYVHKDSEGND--GELFWA
                                                                                                                                                                                                                                                                                                                                                                                                   FVFDECVKAIINVTGLVESGYDDDRGYF-VSSGDTNWGSFKTLFRDHGRVLPGGSCYSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                DPRYPDLVGRGINARFT-PDPDTVRVVATAEQAVRAVQDSVRDGTRLAVR--TGGHCFES 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPRLPSM-KQGFNRRWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGTVRIVSGGHCYED
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            EVNRPGPADTAMAHRDAVLKTYWSVFWFDEREDALHLDWVRASYAEFFGDAGGVPDP
                                                                    LVPDEFAGIKGRFKSKAAFLRTGWSEROARMVYORLTDTSGYHNPA----ATVYLLSHGG
                                                                                              ETING-SGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQVDMFGG
                                                                                                                                                                                                                                                  HTGGGAGSFGLVTRYLFRSPGTDAGSRPADPGRLLPRPPGSVLRKTVRWDWDSVDETAFL
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                                                                                                                                                                                         -VRNFGTWHERHAAPGDPGARLDNSLALPRTGGGPLTLETAVDA 327
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413

364 354 296

282 245 222 200 165 142

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EMBL; U80222; AAD00354.1; -. InterPro; IPR001899; Gram pos anchor. InterPro; IPR001879; Oxid FAD bind. Pfam; PF01855; FAD binding 4; 1
PROSITE; PS00343; GRAM POS ANCHORING; UNKNOWN 1. SEQUENCE 485 AA; 52227 WW; 07DC310677034557
                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces peucetius subsp. caesius.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                    STRAIN=ATCC 27952;
Hong Y.-S., Hwang C.K., Lee J.J.;
"Regulation of anthracycline production in Streptomyces
                                                                                                                                                                                                                                         Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 VESGKGVFEGCYFNYPDVDLNN--WKNGKYGALELYFLGNLNRLIKAKWLWDPNEIFTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGTFINYPDVDLADPRWNTSGVPWYTLYYKGNYPRLORVKARWDPRDVFRHA 482
                   14.7%; Score 440.5; DB 2
28.3%; Pred. No. 1.3e-25;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Mismatches
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                                          DB 2;
183;
                                                                                              CRC64;
                                          Length 485;
Indels
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursjer L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borrilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Odega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Odega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Soffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Yoshida K., Yasamoto H., Yata K.,
Yata M., Yata K.,
Yata M., Yata K.,
Yata M., Yasamoto K., Yata K.,
Yata K., Yata M., Yata K.,
Yata M., Yata K.,
Yata M., Yata K.,
Yata M., Yata M.,
Yata M., Yata M., Yata K.,

                                                                                                                      Query Match
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Matches 144
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01-FEB-1997
01-FEB-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                    EMBL; 282044; CAB04812.1; -.
EMBL; 299108; CAB12708.1; -.
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa Submitted (NOV-1997) to the EMBL/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168
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   41
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                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                   proteome.
                                                           TPDKPDPRLPSMKQGFNRRWIGTNI-----DFVYVVYTPQGACTALDRAMEKCSPGTVR
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(Tremblrel. 02, Last seq
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(Tremblrel. 20, Last ann
54.4 kDa protein (YGAK
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                                                                                                                             Conservative
   ----YNEARTNINLSLERYPDIIVFCQNKQDALNALKWARENRVP--FR
                                                                                                                                                                                                                                                      54477 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ
                                                                                                                                                       13.3%;
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                                                                                                                         66;
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in (YGAK protein).
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                                                                                                                      Score 399; DB 16;
Pred. No. 2e-22;
6; Mismatches 192;
                                                                                                                                                                                                                                                      B43CD118F7FE4C8B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A.;
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                                                                                                                             Indels 152;
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PARECULT PAR
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                           Query Match
Best Local
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FZC5;
                                                                                                       Sakano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B. Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W. Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC TIX7 from Arabidopsis thaliana chromosome 1."; submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC013427; AAF98577.1; -
InterPro; IPR001575; Oxid_FAD_bind.

Pfam; PF01565; FAD_binding 4; 1.

SEQUENCE 530 AA; 58947 MW; 116C6CA06BE4C322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis tihaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T1K7.23 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVSGGHCYEDF-----VFD--ECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHYHLEADIEQIYKTCEPTKALGGHAGWAPFP-----VRPRKRHTSKTSYMHDETMDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFRFEQSIP--PLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFTNKQSIPTKPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFIEAUTFENSPGGNQPQKMKRSGSFIEKPLSERAISTIKHFLEHAPN------QNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFYALTETINGSGPNORGKYK--SAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WDGFTRDALQDLLTKYFKLARCDWKNTVGKFQ1FHQAAEEFVMYLYTSYSNDAEREVAQD
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     Conservative
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                              12.3%;
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76;
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Last annotation updat
                              Score 368.5;
Pred. No. 5.
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
dons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                 3e-20
                                                          DB 10;
        Indels
                                                          Length
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B., Liu A.,
        107;
                                                                                                                                                                                                                                                                                                     C., Lam B.,
Davis R.W.,
        Gaps
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ID Q949N
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                                                  Query Match
Best Local S
Matches 134
                                                                                                                                                             VA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
A Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema B., Lam B.,
A Kin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
A Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Full Length cDNA of gene TIK7.23 (GI:9797759).";
"Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY051000; AAK93677.1; -.
InterPro; IPR001575; Oxid FAD bind.
Pfam; PPF01565; FAD binding_4; 1.

W Hypothetical protein.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Hypothetical 58.9 kDa protein.
TIK7.23.
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Q949N1;
01-DEC-2001
01-DEC-2001
01-MAR-2002
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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VRIVSGGHCYEDFVFDECVKAII-----NVTGLVESGYDDDRGYFVSSGDTNWGSFKT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWLWDPNEIFTNKQSIP 535
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                                                     Conservative
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                                                     76;
                                                  Score 368.5; I
Pred. No. 5.3e-
76; Mismatches
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              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL080254; CAB45SS0.1; -
EMBL; AL161553; CAB79084.1; -
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
SEQUENCE 539 AA; 60143 MW; 6645E9376E21642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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1 (MAR-2000)
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13, Last sequence update)
17, Last annotation updat
                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
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RESULT QSYGT ID VQ9 VG7 ID VQ9 VG7 Q9 DT 011 DT 011
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C OgsvG7;
T 01-MAY-2000 (TrEMBLrel. 13, Created)
T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E Hypothetical 58.8 kDa protein.
E Hypothetical 58.8 kDa protein.
S Arabidopsis thaliana (Mouse-ear cress).
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
C Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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                        SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                               Bevan M., Pohl T., Weizenegger T., Mayer K.F.X., Lemcke K., Schueller Submitted (JUN-1999) to the EMBL/Ge
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                                                                                                                                    Submitted
                                                                                                                                                                                      SEQUENCE FROM N.A.
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omitted (JUN-1999) to the EMBL/GenBank/DDBJ
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d (MAR-2000)
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  CAB45846.1;
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                                                                                                                                  t i
                                                                                                                                  Mewes H.W., Lemcke K., Mayer K.F.X.; the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                          Bancroft I., C.;
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Best Local S
Matches 134
Best
             Query Match
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01-JUN-2001
01-JUN-2001
01-OCT-2001
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InterPro; IPR001575; Oxid FAD
Pfam; PF01565; FAD binding_4;
Hypothetical protein.
SEQUENCE 528 AA; 58846 MW;
                                   "Drought inducible gene from cowpea.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
EMBL; AB056448; BAB3303.1; -
InterPro; IPR001575; Oxid FAD bind.
Pfam; PF01565; FAD binding 4; 1.
SEQUENCE 535 AA; 60291 MW; 7F889FCBF52FD80
                                                                                                                                                             Vigna unguiculata (Cowpea).
Vigna unguiculata (Cowpea).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; V
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                          CPRD2 protein.
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                                                                                                                                                NCBI_TaxID=3917;
Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 VRIVSGGHCYEDFVFDECVK-AIINVTGLVESGYDDDRGY-FVSSGDTNWGSFKTLFRDH
Similarity
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1 (TrEMBLrel.
1 (TrEMBLrel.
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27.0%;
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26.2%;
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Last sequence update)
Last annotation updat
Score
Pred.
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Pred. No. 2.9e-18;
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                               7F889FCBF52FD80E
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 346;
No. :
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2.9e-18;
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                                                                                                                                                               Vigna.
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RESULT 15
Q9FZCE
AC Q9FZCE
AC Q9FZCE
DT 01-MA
DT 01-JU
DE T1K7.
GN T1K7.
GN T1K7.
OS Arabi
OC Eukar
OC Sperm
OC euros
OX NCBI
RN [1]
RP SEQUE
RC STRAI
RA Chin
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                                                                                                                         C STRAIN-CV. COLUMBIA;

R Skano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,

A Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,

Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,

A Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,

A Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,

BCKer J.R., Federspiel N.A., Theologis A.;

"The sequence of BAC TIK7 from Arabidopsis thaliana chromosome 1.";

RT "The sequence of BAC TIK7 from Arabidopsis thaliana chromosome 1.";

RS Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AC013427; AAR98574.1; -.

BR InterPro; IPR001575; Oxid FAD bind.

DR Pfam; PF01565; FAD binding 4; 1.

SQ SEQUENCE 529 AA; 59217 MW; ODC786AA3CB0590D CRC64;
       Query Match
Best Local Similarity
Matches 128; Conserv
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O9FZC8, PRELIMINARY; PRT; 529 AA.
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T1K7.20 protein.
T1K7.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDWLSGVEVVVKPVLTEDSVLKYVHKDSEGN-----DGELFWAHTGGGGGNFGIITKY 215
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11.1%; Score 333.5; DB 10; Length 529; ilarity 25.8%; Pred. No. 2.6e-17; Conservative 77; Mismatches 184; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70; Mismatches 207; Indels 112;
   184; Indels 107;
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vis R.W.,
Gaps
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	72 VI :  103 LF	VRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKT 124 :
,	125 LI 157 KJ	LFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVXPVLTEDSV 182 : :         :  :                :  ::: KINEASQTLAFPAGVCPTVGVGGHISGGGYGNLMRKFGITVDHVSDAQLIDVN 209
•	183 LI	LKYVHKDSEGNDGELFWAHTGGGGGNEGIITKYYFKDLPMSPRGVIASNLHESWDGFT 240
•		
Ĭ	265	TDVLYKWQLVATKFPEDLFMRAWPQIINGAERGDRTIAVVFYAQFLGP 312
,	288 AI	AEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMD 347
	313 AI	ADKLLAIMNORLPELGLRREDCHEMSWFNTTLFWADYPAGTPKSVLLDRPTN 364
Ì	348 YI	YPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDAL-L 406
	365 PC	PGFFTMFKFNNIVWM 400
	407 Q1	QVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYG 465
Ĭ	401 QI	QFNPYGGVMDQIPSTATAFPHRKGNMFKVQYSTTWLAANATEISLSMMKELY-KVAEPY- 458
`	466 GV	GVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAK 519
·	459	VSSNPREAFFNYRDIDIGSNPSDETNVDEAKIYGYKYFLGNLKRLMQVK 507
,	520 WI	WLWDPNEIFTNKQSIP 535
•	508 AI	AKYDPENFFKNEQSIP 523

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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RETO_BAPSO
RETO_ESCCA
MCRA_STRLA
DIVL_CAUCR
MM03_RABIT
YE68_METUA
DLD3_YEAST
YJCS_ECOLI
ELM1_ASPFU
ELM2_ASPFU
DPOM_NEUIUN
MCEL_SFVKA
MM01_BOVIN
AGAB_VIBS7
AIP2_YEAST
AGUA_TRIRE
RF2_BORBU
K1CL_HUMAN
PTP9_DROME
SPEE_AGUAE
CMF2_SCHPO
EST1_CAEEL.
HTRL_ECOLI
DCOR_CHICK
RP01_FOWPV
LRP2_HUMAN
PAPS_BACSU
HN00_ARTOXX
BXB_CLOBO
K6FF_DROME
SXB_CLOBO
K6FF_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
099024 trichoderma
05110 horrella bu
099456 homo sapien
056473 aquifex aeo
P87126 schizosacch
004457 caenorhabdi
P25666 escherichia
P27118 gallus gall
09j593 fowlpox vir
P98164 homo sapien
P42977 bacillus su
P08159 arthrobacte
090611 gallus gall
P10844 clostridium
P52034 drosophila
P28862 mus musculu
                                                                                                                                                                                           P33538 neurospora
P25950 shope fibro
P28053 bos taurus
P48840 vibrio sp.
P46681 saccharomyc
                                                                                                                                                                                                                                                    Q58863 methanococc
P39976 saccharomyc
P32717 escherichia
P46074 aspergillus
P46075 aspergillus
P29761 clostridium
                                                                                                                                                                                                                                                                                                                        P93479 papaver som
P30986 eschscholzi
P43485 streptomyce
O9rqq9 caulobacter
P28863 oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                            Description
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	45	44	43	42	41	40	39	38	37	36	35	34
	89	89	89.5	89.5	89.5	89.5	90	90	90	90.5	90.5	90.5
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ALIGNMENTS	K6P1_YEAST	GAOA_DACDE	TOXB_CLODI	BGAL ASPNG	SYS METMP	MM08_HUMAN	K6P1_PICPA	K6P2_CANAL	NIFD_METMP	RPOB THEMA	HUTU_BACHD	FMO2_HUMAN
	P16861 saccharomyc		P18177 clostridium		O30520 methanococc		Q92448 pichia past	094200 candida alb	P71526 methanococc	P29398 thermotoga	Q9kbe5 bacillus ha	Q99518 homo sapien

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RESULT 2
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DE Enzyme
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P10986;
P10986;
P10986;
P10986;
O1-JUL-1993 (Rel. 26, Created)
O1-JUL-1993 (Rel. 26, Last sequence update)
O1-JUL-1993 (Rel. 26, Last sequence update)
I5-JUN-2002 (Rel. 41, Last annotation update)
Reticuline oxidase precursor (EC 1.5.3.9) (Berberine-bridge-forming Reticuline oxidase precursor (EC 1.5.3.9) (Berberine-bridge-forming Reticuline Oxidase precursor (EC 1.5.3.9)).
                                     SEQUENCE FROM N.A.

MEDLINE-98145481; PubMed-9484487;

Hauschild K., Pauli H.H., Kutchan T.M.;

"Isolation and analysis of a gene bbel encoding the berber enzyme from the California poppy Eschscholzia californica. Plant Mol. Biol. 36:473-478(1998).
                                                                                                                                                                                                                                                                                                                                                                  Eschscholzia californica (California poppy).

Eukaryota; Viridiflantes (Striptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Eschscholzioideae; Eschscholzia.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
MEDLINE=92052284; P.
Dittrich H., Kutcha
                                                                                                                                                                              "Molecular cloning, expression, and induction of berberine bridge enzyme, an enzyme essential to the formation of benzophenanthridine alkaloids in the response of plants to pathogenic attack."; proc. Natl. Acad. Sci. U.S.A. 88:9969-9973(1991).
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                                                                                                                                                                                                                                                               2284; PubMed=1946465;
Kutchan T.M.;
    'n
                       Essential to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Pred. No. 7.5e-15;
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  pathogenic
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                       benzophenanthridine
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF005655; AAC39358.1; --
PIR; A41533; A41533.
InterPro; IPR001575; Oxid FAD
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PROSITE; PS00862; ÖX2 COVAL FAD; 1.
Oxidoreductase; Signal; Glycoprotein; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S65550; AAB20352.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Benzophenanthridine alkaloids SUBCELLULAR LOCATION: VESICULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catalyzes the stereospecific conversion of the N-methyl moiety of (S)-reticuline into the berberine bridge carbon of (S)-scoulerine CATALYTIC ACTIVITY: (S)-reticuline + O(2) = (S)-scoulerine + H(2)O(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidoreductase family.
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    ISRSWGESYFLSNYERLIRAKTLIDPNNVFNHPQSIP
                                                                                   LDWLEKVYEFM-KPF---VSKNPRLG-----YVNHIDLDLGGIDWGNKTVVNNAIE
                                                                                                                         LKWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLN--NWKNGKY--GALE
                                                                                                                                                                                                   PDGLTSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYI-IKLQYQTYW--QEEDKDAVN
                                                                                                                                                                                                                                                                                  RHTSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEV
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                           YFLGNLNRLIKAKWLWDPNEIFTNKQSIP
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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Pred. No. 1.5e-14;
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01-NOV-1995
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and analysis of a locus (mcr) involved resistance in Streptomyces lavendulae.";
J. Bacteriol. 176:4448-4454(1994).
-!- FUNCTION: INVOLVED IN MITOMYCIN RESISTANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L29247; AAA21476.1; -. InterPro; IPR001575; Oxid_FAD_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: BY MITOMYCIN C IN CONCENTRATIONS AS LOW AS 300 NM
-!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF MITOMYCINS.
-!- COFACTOR: FAD (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces lavendulae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitomycin radical oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01565; FAD binding 4; 1.
PROSITE; PS00862; OX2 COVAL FAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
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NCBI_TaxID=1914;
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                   309
                                                223 VPEEMASSVLLVHNPDLPDVPEPLRGRFITHLRIAYSGE-
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                                                                                                                                                                                                                                                                  78 GHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGS
                                                                                                                                                                                                                                                                                                                                21 PDKP---DPRLPSMKQGFNRRWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGTVRIVSG
                                                                                                                                                                                                                                                                                                                                                               85;
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KTCEPTKALGGHAGWAPFPV---RPRKRHTSKTSYMHDETMDYPFYALTETINGSGPNQR: | ; | | | ; |
                                                                                                                                          FWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARC
                                                                                                                                                                         SPNVGAVGYLVGGGAGLLGRRFGYAADHVRRLRLV----TADGRLRDV---TAGTDPDL
                                                                                                                                                                                                      CYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGEL
                                                                                                                                                                                                                                       GH-GPSVSADDAV--LVNTRRMEGVSVDAARATAWIEAGARWRKVLEHTAPHGLAPLNGS
                                                                                                             FWA-VRGGKDNFGLVVGMEVDLFPVT--RLYGGGLYFA----GEATAEVLHAYAEWVRH
                                                                                                                                                                                                                                                                                                                                                                                                                   63
447 AA;
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(Rel., 32, Last sequence update)
(Rel. 41, Last annotation updat
(Rel. 41, Cast annotation)
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                   -GLNRA-AESRPAYVVEAADEQEVAAAVRLAAEQKRP--VGVMAT
                                                                                                                                                                                                                                                                                                                                                             51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Score 154.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                             FAD (COVALENT)
                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                           AD (COVALENT) (BY SIMILARITY).
3B0071BB818D838C CRC64;
                                                                            AAEEFVMYLYTSYSNDAEREVAQDRHYHLEADIEQIY
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                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                               163; Indels 81;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 447;
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A Nierman W.C., Peldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

A Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Witerback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

C -! PUNCTION: Required for cell division and growth It catalyzes the

C phosphorylation of Ctra and activates transcription in vitro of

the cell cycle-regulated flip promoter.

SIBCELIULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPROQ9; Q9A2S2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sensor protein divL (EC 2.7.3.-)
                                               Pfam; PF02518; HATPase_c; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKA; T.
TIGREPANS; TIGR00229; sensory_box;
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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MEDLINE=20027501; PubMed=10557274;
Wu J., Ohta N., Zhao J.L., Newton A.;
"A novel bacterial tyrosine kinase es
                PROSITE; PS50109; HIS_KIN; 1. Sensory transduction; Transferase;
                                                                                                                                                          InterPro; IPR004358; Bact sens_pr_C.
InterPro; IPR003661; His_KIN_A.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR004014; PAS_domain.
                                                                                                                                                                                                                                    PhosSite; Q9RQQ9;
                                                                                                                                                                                                                                                                      EMBL; AF083422; AAF08344.2; -. EMBL; AE006007; AAK25446.1; -.
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-!- SIMILARITY: CONTAINS 1 |
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STRAIN=ATCC 19089 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 96:13068-13073(1999).
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P28863;
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                    homology with stromelysin and with collagenase.";
                                                             "Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase that activates synovial cell collagenase.
                                                                                                          Fini M.E., Karmilowicz
Brinckerhoff C.E.;
                                                                                                                            MEDLINE=88077214; PubMed=2825726; Fini M.E., Karmilowicz M.J., Ruby P.L.,
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                          MMP3
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or (EC 3.4.24.17) (Matrix
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HISTIDINE KINASE.
ALA-RICH.
PHOSPHORYLATION ()
Q -> H (IN REF. 1)
Q -> E (IN REF. 1)
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Pred. No. 0.23;
                                        transin,
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                                        and is coordinately regulated
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                                                                                                                              K.A.,
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SEQUENCE OF 1-167 FROM N.A.
MEDLINE=87156645; PubMed=3030290;
Whitham S.E., Murphy G., Angel P., R
Whitham A., Harris T.J.R., Reynolds J.
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Pfam; PF000113; Peptidase M10; 1.
PRINTS; PR00138; MATRIXIN.
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMC; 1.
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PROSITE; PS00546; CYSTEINE SWITCH; 1.
Hydrolase; Metalloprotease; Glycoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Matrixin.
InterPro; IPR000130; Zn_MTpeptd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There by non-profit institutions as long as modified and this statement is not removed. I entities requires a license agreement (See httentities requires a license agreement)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence analysis.";
Biochem. J. 240:913-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Lyons A., Harris T.J.R., Reynolds J.J., Herrlich P "Comparison of human stromelysin and collagenase b
                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                             Collagen
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                                                                                                                                                 Similarity
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IV, AND V; COLLAGENS III, IV, X, AND IX,
EOGLYCANS. ACTIVATES PROCOLLAGENASE.
                                                                 GLVES-GYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILA
                                                                                                             RWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVT
                                                                                                                                                                                                                                                                                                                                             degradation;
                      RLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYY
                                                                                         KWTKTHLTYRIVNYTPDLPRDAVDAAIEK-----
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Extracellular matrix; Signal.
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ZINC (CATALYTIC) (I
LINKED (GLCNAC.
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N -> D (IN REF.
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                                                                                                                                                Score 116; DB Pred. No. 0.19;
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(BY SIMILARITY).
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by cloning and
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[IGR; MJ1468; -.
InterPro; IPR000601; PKD_uu...
Pfam; PF00801; PKD; 6.
SMART; SM00089; PKD; 7.
PROSITE; PS50093; PKD; 5.
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MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: Integral memb:
-!- SIMILARITY: CONTAINS 5 PKD DOMAINS.
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                                                                                                                                                                                                                                                              EMBL; U67588; AAB99478.1; TIGR; MJ1468; -.
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1 protein MJ1468.
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Matches 113;
                                                                                                                                                                                                                           DLD3 FEAST STANDARD; PRT; 496 AA. P39976; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Probable D-lactate dehydrogenase (cytochrome) ferricytochrome C oxidoreductase) (D-LCR). DLD3 OR YELO71W.
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                 Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT eptry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Flavoprotein; FAD.
SEQUENCE 496 AA; 55225 MW; 480
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COFACTOR: FAD (POTENTIAL).
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                                                                                                                                                                                                                         KDFPDFQIDVIWKYLTEVPDGL------TSAEMKDALLQVDMFG--
                                                                                                                                                                                                                                                                                                                                    RKRHTSKTSYMHDETMDYPFYALTETINGSGPNQRGK---
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RESULT 8
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                                                                                                                                                                                                                                                               Matches 117;
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Best Local :
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15-JUL-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as in modified and this statement is not removed. Us entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=94089392; pubMed=8265357;
Belattrer F.R., Burland V.D., Plun
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Pfam; PF00753; lactamase B; 1.

Hypothetical protein; Complete proteome.

CONFLICT 614 614 H -> D (IN REF. 1)
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Nucleic Acids Res. 21:5408-5417(1993).
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                  DVNAGTPDKPDPRL--PSMKQGFNRRWIGT-----NIDFVY------VVY 51
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          Markaryan A., Morozova I., Yu H., Kolattukudy P.E.;
"Purification and characterization of an elastinolytic
metalloprotease from Aspergillus funigatus and immunoelectron
microscopic evidence of secretion of this enzyme by the fungu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sirakova T.D., Markaryan A., Kolattukudy P.E.;
"Molecular cloning and sequencing of the cDNA and gene for a novel
elastinolytic metalloproteinase from Aspergillus fumigatus and its
expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
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01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Extracellular elastinolytic metalloproteinase
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                                                                                                                                                                                                                                                                                                                                                                Infect.
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                                                                                                                                                                                                                                                                -!- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus (Sartorya fumigata)
                                                                                                                                                                                                                                                                                                                                                                                                  invading
                                                                                                                                                                                                                                                            ading the murine lung.";
ect. Immun. 62:2149-2157(1994).
FUNCTION: CATALYZES THE HYDROLYSIS OF ELASTIN.
COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
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                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  Sanglard D.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
-!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M36.
                                                                                                                                                                                                                                                                                                                                                                                                   Jaton-Ogay K., Paris S., Huerre M., Quadroni Togni G., Latge J.-P., Monod M.;
"Cloning and disruption of the gene encoding metalloprotease of Aspergillus fumigatus.";
Mol. Microbiol. 14:917-928(1994).
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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                                                                                                                                                                                                                                                                                                                               STRAIN=DELTA18;
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itosporic Trichocomaceae; Asperg
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                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                                                                    a collaboration -
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RESULT 11

AMYG CLOSP
ID AMYG C
AC P29761
DT 01-APR
CCA CLOST
RAM (11)
RP SEQUEN
RA OMNISH
RT "MOLEC
RT EUX. J
CC -!-FU
CC -!-FU
CC -!-FU
CC -!-SU
CC -
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                                                                                                                                                                                                                            A Chrishi H., Kitamura H., Minowa T., Sakai H., Ohta T.;

(A) Chrishi H., Kitamura H., Minowa T., Sakai H., Ohta T.;

(T) Clostridium and kinetics of the cloned enzyme.";

(C) Clostridium and kinetics of the cloned enzyme.";

(E) Eur. J. Biochem. 207:413-418 (1992).

(C) -!- FUNCTION: CGA HAS TYPICAL KINETIC PROPERTIES FOR A GLUCOAMYLASE,

(C) -!- FUNCTIVITY THAN OTHER EUKARYOTIC GLUCOAMYLASES.

(C) -!- CATTALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-

(C) CATTALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-

(C) Glucose residues successively from non-reducing ends of the chains

(C) Glucose residues funcasively from non-reducing ends of the chains

(C) -!- SUBCELLAURACUS: HIGH ACTIVITY TOWARDS 1,6-GLYCOSIDIC BONDS.

(C) -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
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P29761;
01-APR-1993
                       entities
or send a
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ACT_SITE
METAL
                                                                                                                                                       This SWI
between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001842; Fungalysin.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF02128; Peptidase M36; 1.
PRINTS; PR00999; FUNGALYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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MEDLINE=92339427; PubMed=1633799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ostridium.
                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
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                       non-profit institutions as lond and this statement is not remove requires a license agreement (S. an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVAEADYQVYAWGINDPTEGERTVIKDPWDSVASEFTWISDGSTNYTTSRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMIKDFPDFQIDVIWKYLTEVPDG--LTSAEMKDALLQVDMFGGEIHKVVWDATAVAQRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain G0005).
outes; Clostridia; Clostridiales;
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; Pred. No. 3.3;
26; Mismatches
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ZINC (CATALYTIC) (E
BY SIMILARITY.
ZINC (CATALYTIC) (E
                                                                          is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702
                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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Probable DNA polymerase (EC Neurospora intermedia, Mitochondrion.

Plasmid

kalilo

P33538; 01-FEB-1994 01-FEB-1994 15-DEC-1998

(Rel. 28, Created)

(Rel. 28, Last sequence update) (Rel. 37, Last annotation update)

2.7.7.7).

RESULT 12 DPOM\_NEUIN

DPOM\_NEUIN

STANDARD;

PRT;

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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000165; GH 15.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
PROSITE; PS00820; GLUCOAMYLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JQ0868; JQ0868.
PIR; S24140; S24140.
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487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                    FIVTDG---KSFVSDETKDTI----SKVEKFTDKSLGYKLVNTDKK-GRYRITKEIFTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                PDKPDPRLPSMKQGFNRRWIGTNIDFVYVVY--TPQGACT----ALDRAMEKCSPGTVR
SAQKYQEKADNWQKLIDNLTYTEHGPLE----NGQYYIRIAGLPDPNADFT
                                                                                                                A-EMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQ-EEDKDAVNLKW----
                                                                                                                                                               YMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIW-KYLTEVPDGLTS
                                                                                                                                                                                                                                  SIGYYKVNDIMTDLDENKOMTKHYDSAR---GNIIEGAEIDLKKNSOFEIVLSFGNSEDE
                                                                                                                                                                                                                                                        T-----RDALQDL-----LTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSND-
                                                                                                                                                                                                                                                                            LEGSIHDYKLYLAYDPHIKNQGSYNEGYVIKANNNEMLMAKRDNVYTALSSNI--GWKGY
                                                                                                                                                                                                                                                                                                     SEG--NDGELFWAH----TGGGGGGNFGIITKYYFKDLPMSPRG----VIASNLHFSWDGF
                                                                                                                                                                                                                                                                                                                                                     GRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKD
                                                                                                                                                                                                                                                                                                                                                                                                  -IVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSF---KTLFRDH 129
                       ----- LNWKN-----
                                              YDLYDSLVKPLADFIIKMGPKTGQERWEEIGGY-SPATMAAEVAGLTCAAYIAEQNKDYE
                                                                                           AGDVDSANRSLDY----LAKVVKDNGMIPONTWISGKPYWTGIOLDEQADPIILSYRLRR
                                                                                                                                        YI--ASLSIPWG-----DGQGDDNTGGY------HLVWSRDLYHVANAFIA
                                                                                                                                                                                                                                                                                                                                                                                                                          PGEEDTWASAQKQG-----VGTANNYVSKVWFTLANGAISEVYYPTIDTADVK----EIK
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                                                                   --IRDFY-----EEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVD--
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455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polysaccharide degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-ACYL DIGLYCERIDE (PROBABLE).
SUBSTRATE (BY SIMILARITY).
CATALYTIC BASE (BY SIMILARITY).
GENERAL ACID CATALYST (BY SIMILARITY).
INTERACT WITH SUBSTRATES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
GLUCOAMYLASE.
                     -GKYGALELYFLGNLNRLIKAKWLWDPNEIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      955EB4D0AD569546 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein;
                                                                                                                                                                                                                                                                                                                              -VKRNSLIMKAKFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184;
  533
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                                                                                                                                                                                                                                                                                                                               158
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mRNA

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RESULT 13
MCEL_SFVKA
ID MCEL_SFVKA
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Matches 76
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PIR, S17909; S17909;
InterPro; IPR00264; DNA_pol_B.

InterPro; IPR004868; DNA_pol_B 2.

PEAm; PF03175; DNA pol_B 2; 1.

PRINTS; PR01016; DNAPOLB.

SMART; SM00486; POLBC; 1.

SMART; SM00486; POLBC; 1.

Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Plasmid; Mitochondrion.

SEQUENCE 969 AA; 112829 MW; 6048B993814F668F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=92035090; PubMed=1934129;
Chan B.S.S., Court D.A., Vierula P.J., Bertrand I
"The kalilo linear senescence-inducing plasmid o
invertron and encodes DNA and RNA polymerases.";
Curr. Genet. 20:225-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5142;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            EQIYKTCEPTK----ALGG--HAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKFQIFHQAAEEFVMYLYTSYSNDAER-----EVAQDRHYHLEADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKYYFKDLPMSPRGVIASNLHFSW------DGFTRDALQDLLTKYFKLARCDWKNTV
                                                                                                                                                              VFENGEMVFFSENVKTSFIKKITRODLINFENPKIITLDL-
                                                                                                                                                                                               QVESGKGVF--EGCYFNY----PDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDPNE
                                                                                                                                                                                                                                ITINKKYNEITVLLNNTPIFKIKDEKIMSEDDLSSFKRTITENEODKVY------
                                                                                                                                                                                                                                                                       GEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNT
                                                                                                                                                                                                                                                                                                                                        GSGPNQRGKYK-SAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQ-VD----MFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKFYSTSTD-SPMGHIVSASKSSWYNYYSHKNYDPLTRESFHDELRGFISLYKKQFKE--
                                                                                                                               I FTNKOS I PTKPLKEPKOTK
                                                                                                                                                                                                                                                                                                          LSKKNPLNKFKYNGYTIPNTMDLS---QWPNIHFINDGKNAVSLNNIIKSGVDNMTLSFF
                                                                                                                                                                                                                                                                                                                                                                                SE--AVSEPFEYELFSLGDGLPKGNIIFTFKPTSNPSIKTKYEHKSNI-----KRNKNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EKFFFMAKIKFNNNDIRSISTVQIGSTDPLEVLRLLEAITSTYMHTHTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 101.5; ilarity 20.0%; Pred. No. 6.3; Conservative 50; Mismatches
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA POLYMERASE REQUIRES A PROTEIN
       PRT;
       836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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of Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  969;
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Upton C., Stuart D., McFadden G.;
"Identification and DNA sequence of the large subunit of the capping enzyme from Shope fibroma virus.";
Virology 183:773-777(1991).
-!- FUNCTION: CAPTAYZES THE FIRST TWO REACTIONS IN THE MRNA CAP FORMATION PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P25950;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
mRNA capping enzyme large subunit [Includes: Polynucleotide 5'-
triphosphatase (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); m
guanylyltransferase (EC 2.7.7.50) (GTP--RNA guanylyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03291; Pox_MCEL; 1.
Transferase; Nucleotidyltransferase; Hydrolase; mRNA capping; Multifunctional enzyme.
ACT_SITE 256 GUANYLYLATION SITE SEQUENCE 836 AA; 97018 MW; 7375FDA548AE1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M63902; AAA47224.1; -. PIR; A40478; QQVZRA. InterPro; IPR004971; Pox_MCEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shope fibroma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91306463; PubMed=1649507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shope fibroma virus (strain Kasza) (SFV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: 5'-phosphopolynucleotide + H(2)O polynucleotide + phosphate. 
CATALYTIC ACTIVITY: GTP + (5') PP-pur-mRNA = diphospha G(5') PPP-pur-mRNA. 
SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT. 
SIMILARITY: BELONGS TO THE VIRAL GTASE FAMILY.
                                      307
                                                                                                                                               507
                                                                                                                                                                               198
                                                                                                                                                                                                                    462
                                                                                                                                                                                                                                                                                        413
                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                               28 LPSMKQGFNRRWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGTVRIVSGGHCYEDFVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                     VGLGGHIVGGGDGILARLHGLPVDWLSGVEV---VVKPVLTEDSVLKYVHKDSEGNDGEL
       LVATDPDKEAIG-
                                                                                                                                                                                                                                                                                        E----NSTFLEYKKFSDDKGF----PKDYGTGKLMLTDNVRYLNNIYCIAFTNVYED
                                                                                                                                                                                                                                                                                                                         ECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYS-----
                                                                                                                                                                                                                                                                                                                                                              LPSQPEG-----VVLFYSDQRNQPDYKIKLDNTTDHMINIIYRYMSSEPVIFG
                                      IYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETING----
                                                                                                            CDWKNTVGKFQIFHQAAEEFVMYLY---TSYSNDAEREV-----AQDRHYHLEADIEQ
                                                                                                                                               VVAHIRDQNIKIGDVLDEDKLSDV------GQHYANDKYRLNPDVSYFTN-----
                                                                                                                                                                               FWAHTGGGGGNFG-IITKYYFKDLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLAR
                                                                           --- KRTRGPLGILSNYVKTLLISLYCSKTFLDNSNKRKVLAIDFGNGADLEKYFYGEISS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97.5; DB 1;
Pred. No. 11;
5; Mismatches 169;
                                                                                                                                                                                                                    PIKFISEFSATGELIKPRI--DKTFKYLYKEYYGNQYQI
       RCIERYNSLNSGI--KSKYYKFDYIQETIRSVTYVSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 141;
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Gaps

412 87

140

197

256 506

550

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Pfam; Frotal;
PRINTS; PRO0138; MATRIXIN.

SMART; SM00120; HX; 4.

SMART; SM00125; ZnMC; 1.

PROSITE; PS00024; HEMOPEXIN; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00546; CYSTEINE SWITCH; 1.

PROSITE; PS00546; CYSTEINE SWITCH; 1.

WHydrolase; Metalloprotease; Glycoprotein; Zinc; Zymoge: Wight and Collagen degradation; Extracellular matrix; Signal.

W Collagen degradation; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P28053;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
Interstitial collagenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM01_BOVIN
P28053;
                                                                                                                                                         InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00045; hemopexin; 4.
Pfam; PF00413; Peptidase M10; 1.
PRINTS; PR00138; MATRIXIN.
                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOVIN
                                                                                                                                                                                                                                                                                                   EMBL; X58256; CAA41210.1; -. PIR; S14654; KCBOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95201294; PubMed=7894061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                             InterPro; IPR000585; Hemopexin
InterPro; IPR001818; Matrixin.
                                                                                                                                                                                                                                                                  MEROPS; M10.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of bovine interstitial collagenase deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Periodontium fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVATION PEPTIDE.
SIMILARITY: BELONGS TO
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-|-11e<sup>4</sup>776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a budgaranchic collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydrophobic residue.
COFACTOR: REQUIRES CALCIUM AND ZINC ENZYME REGULATION: CAN BE ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq. 5:63-66(1994).
FUNCTION: CLEAVES COLLAGENS OF TYPES I, II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          709
                                                                                                                                                                                                                                                                                    P03956; 1HFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSQLTDKKTFVIHKNLPSSENYMSVEKIHEDQILVXNPSSMSRPMQEYIVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NQ----RGKYKSAYMIKDFPDFQIDVIW----KYLTEVPDGLTSAEMKDALLQVDMFGGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimokawa H., Sasaki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemopexin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDASE FAMILY M10A. HEMOPEXIN-LIKE DOMAIN.
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                                                      Calcium;
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RESULT 15
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SITE
         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                   Vibrio sp. strain JT0107.",

Biochim. Biophys. Acta 1218:105-108(1994).

FUNCTION: HYDROLYZES AGAROSE TO YIELD PREDOMINANTLY

NEOAGAROTETRAOSE AND NEOAGAROHEXAOSE.

CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-galactosidic linkages
in agarose, giving the tetramer as the predominant product.

SIMILARITY: BELONGS TO FAMILY 50 OF GLYCOSYL HYDROLASES.
                                                                                                                                                              MEDLINE=94250684; PubMed=8193156;
Sugano Y., Matsumoto T., Noma M.;
"Sequence analysis of the agaB gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
CHAIN
                                                                                                                                                                                                                   NCBI_TaxID=47913;
                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                        Vibrio sp.
                                                                                                                                                                                                                                                               Beta-agarase
                                                                                                                                                                                                                                                                           01-FEB-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                               P48840;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                       between
                                                               This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      AGAB_VIBS7
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                                                     the Swiss Institute of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TIRGEVMFFKDRF---
                                                                                                                                                                                                                               Proteobacteria; gamma
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469
                                                                                                                                                                                                                                            (strain JT0107).
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(Rel. 33, Last sequence update)
(Rel. 34, Last annotation update)
B (EC 3.2.1.81).
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Pred. No.
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ZINC (CATALYTI
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CYSTEINE SWITCH
ZINC (CATALYTIC)
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                                                       Bioinformatics
                                                                                                                                                                                                                                 subdivision; Vibrionaceae; Vibrio
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           (See http://www.isb-sib.ch/announce/
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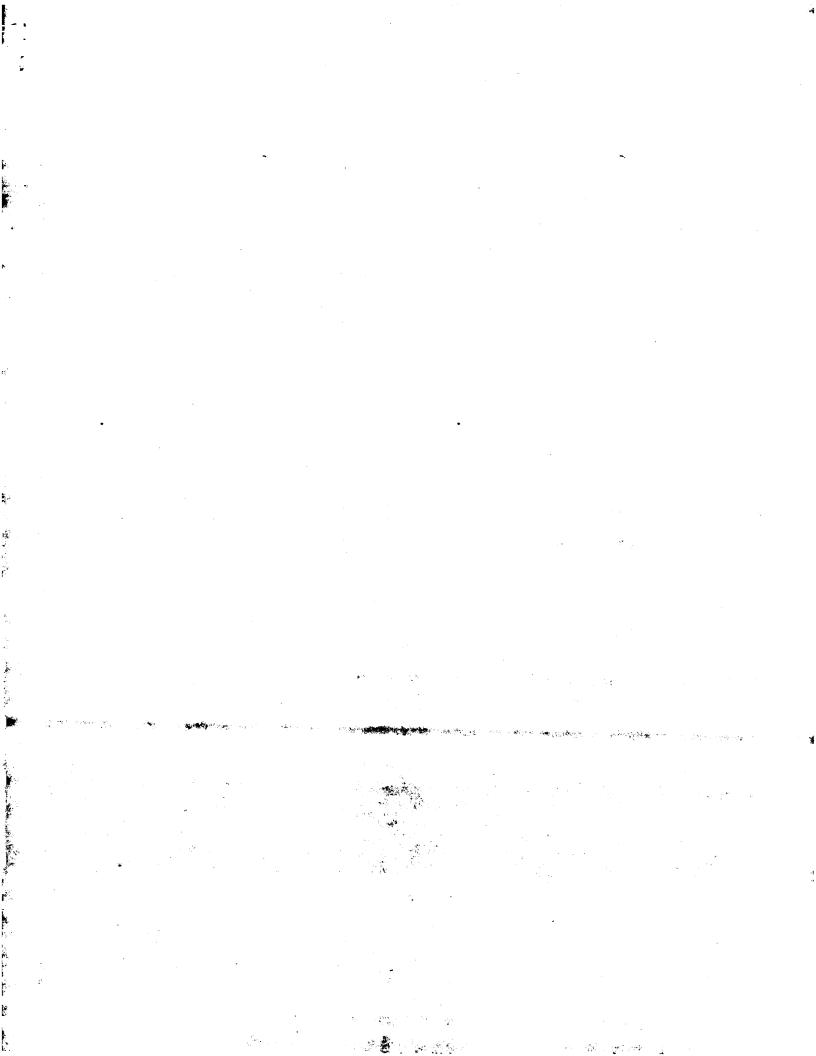
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license@isb-sib.ch)

1000年

SQ R	EMBL; D21202; BAA04744.1; Hydrolase; Glycosidase; Multigene family. SEQUENCE 955 AA; 105976 MW; 6E54555DDA8BD215 CRC64;
Que Bes Mat	Query Match 3.2%; Score 97; DB 1; Length 955; Best Local Similarity 20.5%; Pred. No. 14; Matches 56; Conservative 46; Mismatches 97; Indels 74; Gaps 16;
Ş	104 YDDDRGYFYSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPV 163
đđ	629 YDNKKVAYVANGWIFGDHARISTGNDYWGPIHD-PF 663
8	164 DWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYY 216
문	664 DPEFVNSVKAMTKKLMTEVDKNDPWMMGVFVDNEISWGNTKNDANHYGLVVNAL 717
Ş	217 FKDLPMSP-RGVIASNLHFS-WDGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAE 274
문	718 SYDMKKSPAKAAFTEHLKEKYWAIEDLNTSWGVKVASWAEFEKSFD 763
δ	275 EFVMYLYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPV 328
망	764HRSRISKNMKKDYAEMIEMISAKYFSTVRAEIKKVIPNHIYIGAPFADWGV 814
Ş	329 RPRKRHTSKTSYMHDETMDYPFYALTETINGSG 361
뮍	815 TPEIAKGAAPYVDVMSYNLYAEDLNSKG 842

Job time : 27 secs



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Post-processing: Minimum Match
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Listing first 45 summaries
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AG0038
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chilingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Genome sequence of Yersinia pestis, the causative agent of plague. A,Reference number: AB0001; MUID:21470413; PMID:11586360 A,Accession: AG0038
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C;Genetics:
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A; Residues: 1-685 < KUR>
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Best Local Similarity
Matches 195; Conserv
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               335 NIPPFKHLYPGRKIGRTVDESASMDWLHVTQMINGSGSNQRGKYKSDYQIKQFSD---EM
                                                                                                                                                                                                                                                                                                    56 ITVR--SGGHCYEGFVSNKLSTERLSIIDLGEMSGLDYDEDKTITSLWDANKNTYRFKSL
                                                                                                                                                                                                                                                                                                                               70 GTVRIVSGGHCYEDFVFDECVKAIINVTGLVE-SGYDDDRGYFVSS-------
                                                                                                                                                                                                                                                                                                                                                                                         13 VIDVNAGTPDKPDPRLPSMKQGFNRRW---IGTNIDFVYVVYTPQGACTALDRAMEKCSP
                                                                                                                                                                                                                                                                                                                                                            3 IIDKNVSTYB-----TLQKGFNLRWPPNVEQGAETIYICTTPDEVFAATNTALAAGNR
                                                                                                                                                         HFSWDGFTRDALQDLLTKYFKLARCDW------KNTVGKFQIF-----H-QAAE
                                                                                                                                                                                    PVGNAHRLAFRHVRADSVSEVDRELLMACCGAGGGNFGIIIAYYFDDLPKAPQKAYWIPL
                                                                                                                                                                                                      KPVLTEDSVLKYVHKDSEGN-DGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNL
                                                                                                                                                                                                                                                         -GDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVV
                                        VRPRKRHT---SKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDV
                                                                                              EFVMYLYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAP------FP
                                                                                                                            TYPW-----SSLKATFPAFLK-AYWQWFADNDVNATSTKEGVGNGGLFTLLKLNHIDASD
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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33.6%; Pred. No. 3.2e-48;
rative 77; Mismatches 205;
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B97033
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Gaps

4. B.

113

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391

334 327 287 274 233 55

Result No.

Score

Length

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% Query Match

347.5 347.5 347.5 347.5 337.5 332.5 332.5 332.5 302.5

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Searched:

Scoring table: Sequence:

BLOSUM62

Gapop 10.0 ,

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Title: Perfect score:

Run on: OM protein -

Copyright

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R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Worder, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
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C; Superfamily: po
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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A; Residues: 1-530 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 12.3%; Score 368.5; DB 2; Similarity 27.0%; Pred. No. 3.1e-20;
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VPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGK-----YGALELYFLGNLNRLIKA
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                                                            FNPYGGVMDRIPATATAFPHRKGNLFKIQYFTTWFNANATMSSLSQMKELY-EVAEPY--
                                                                                             VDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGG 466
                                                                                                                                                                                                                   TDALMAIMNONWPELGLK--HEDCQEMSWLNSTLFWADYPA-----GTPTSIL----LD
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                                                                                                                                                                          YPFYALTETINGSGPNQRGKYKSAYMIKDPPDFQIDVIWKYLTEVPDGLTSAEMKDALLQ 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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C; Date: 05-Dec-1997
C; Accession: F69816
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A; Residues: 1-367 < KUN>
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A;Residues: 1-367 <KUN>
A;Residues: 1-367 <KUN>
A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12708.1; PID:e1182869; A;Experimental source: strain 168
C;Genetics:
A;Gene: ygaK
A;Gene: ygaK
Query Match
Best Local Similarity 26.0%; Score 360.5; DB 2; Length 367;
Best Local Similarity 26.0%; Pred. No. 7.5e-20;
Matches 118; Conservative 61; Mismatches 157; Indels 117; Gaps 15;

166 LSGVEVVVKPVLTEDSVLKYVHKDSEG-----NDGELFWAHTGGGGGNFGIITKYY 216 106 DDRGYFVSSGDTNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDW 165 FLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK 540 ----WPPYTDD-----PKTELKKLLK 185 VMYLYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFP-----VR FKDLPMSPRGVIASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEF 276 ---NVERLRRVKTTYDPENVFRFEQSIP---PLR VNLKWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGKYGALELY 507 FLEHAPN-----QNASVWQQALGGAAGRVAPDQTAFYYRDAIIAQEYLTNWTSPGEKR YLTEVPDGLTSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDA PLLKAGSPTSGMVKTT--PRKRHTSKTSYMHDETMDYPFYALTETINGSGPNQRGKYK--SAYMIKDFPDFQIDVIWK FKAVPISQUSIF--SITWGWDDFEE--LVQLEMIVA-----DEKEGADLITVSCSNHPDLFWASQGGGGGFGIVTSMT DKKLAYIEAGAELGEVYRTLWQ-YGLTLPAGTIANVGLTGLTLGGGIGLLTRAAGLTCDS - PFIEAVTFFNSPGGNOPOKMKRSGSFIEKPLSERAISTIKH -TMGDYVNWPDIEIRNWPRTYYGE----362 ---VYNTWQN---329 334 295 242 144 67

C:Accession: T10626 R:Bevan, M.; Pohl,

RESULT

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reticuline oxidase homolog F21C20.190 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 15-Jun-2001

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Mon J)

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A,Reference number: Z16991
A,Reference number: Z16991
A,Rocession: T10626
A;Molecule type: DNA
A,Residues: 1-539 <BEV>
A;Cross-references: EMBL:AL080254; GSPDB:GN00062; ATSP:F21C20.190
A,Experimental source: cultivar Columbia; BAC clone F21C20
C;Genetics:
A;Genetics:
A;Gene: ATSP:F21C20.190
A;Map position: 4
C;Superfamily: poppy reticuline oxidase
hypothetical protein F21C20.150 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Jun-2001 C;Accession: T10622 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K submitted to the Protein Sequence Database, June 1999 A;Reference number: Z16991 A;Accession: T10622 A;Molecule type: DNA
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Pred. No. 1.3e-18;
6; Mismatches 181
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                                                                                  K.F.X.;
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                                                                                  Lemcke
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Mewes, H.W.; Mayer, K.F.X.; Lemcke
                                                hypothetical protein T1K7.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86.91
C;Accession: A86.91
C;Accession: A86.91
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I.
ansen, N.F.; Hughes, B.; Huizar, L.
Asture 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86391
A;Status: preliminary
A;Residues: 1-529 < STO>
A;Residues: 1-529 < STO>
A;Residues: 3-529 < STO>
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A;Cross-references:
C;Genetics:
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                            GB:AE005172; NID:g9797756; PIDN:AAF98574.1;
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ewar, K.;
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hypothetical protein TIK7.24 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: E86390
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.AAuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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E86390
                                                                                                        A; Map position:
C; Superfamily: |
                                                                                                                                                  A; Cross-references: C; Genetics:
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A; Residues: 1-535 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDALQDLLTKYFKLARCDWKNTVGKF--QIFHQAAEEFV------MYLYTSYSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPR--GVIASNLHFSWDGFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINEASQTLAFPAGVCPTVGVGGHISGGGYGNLMRKFGITVDHVSDAQLI-----DVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFRDHGRVL--PGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRIRSGGHDLEGLSYRSSVPFVILDMFNLRSITVNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRIVSGGHCYEDFVFDECVKAII-----NVTGLVESGYDDDRGYFVSSGDTNWGSFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLWDPNEIFTNKQSIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDAL-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLLNRASMGED--LFWAIRGGGGASFGVILSWKI-NLVKVPKILTVFKVNKTLEQGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFNPYGGVMDQIPSTATAFPHRKGNMFKVQYSTTWLAANATEISLSMMKELY-KVAEPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADKLLAIMNQRLPELGLRR--EDCHEMSWFNTTLFWADYPAGTPK-----SVLLDRPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TDVLYK-----WQLVATKFPEDLFMRAWPQIINGAERGDRTIAVVFYAQFLGP
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                                                                                                                                                                      GB:AE005172; NID:g9797760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSSNP---REAFFNYRDIDIGSNPSDETNVDEAKIYGYKYFLGNLKRLMQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 333.5; DB 2; 25.8%; Pred. No. 1.5e-17; rative 77; Mismatches 184;
                                           11.0%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77;
                                                                                                           oxidase
                        66;
                                           Score 328.5; DB 2
Pred. No. 3.6e-17;
                          Mismatches
                                                                                                                                                                        PIDN:AAF98578.1; GSPDB:GN00141
                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KKAWVQAGAT-LGELYV
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                        25
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait C.A.; Li, J.H.; Lin, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Fitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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(B86151

(B86151)

(F22M8.11 protein - Arabidopsis thaliana

(C;Species: Arabidopsis thaliana (mouse-ear cress)

(C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change

C;Accession: G86151
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C; Superfamily: I
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A; Residues: 1-541 <STO>
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120 GSFKTLFRDHG-RVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 L-LQVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKLLNRSTMGED--LFWAIRGGGGASFGVILSWKI-NLVEVPKIFTVFQVNKTLEQGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFRDHGRVL--PGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGK-----YGALELYFLGNLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWLHFNPYGGMMDRIPSNATAFPHRKGNLFKVQYYTTWLDPNATESNLSIMKELY-EVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-DPVFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QFLGRTDELMEIMNQSFPELGLRREDCQEMSWLNTTLFWAMLPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKYVHKDSEGNDGELFWAHTGGGGGGNFGIITKYYFKDLPMSPR--GVIASNLHFSWDGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIDEASQTLAFPAGICATVGAGGHISGGGYGNLMRKFGTTVDHVIDAELV-----DVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRIVSGGHCYEDFVFDECVKAII-----NVTGLVESGYDDDRGYFVSSGDTNWGSFKT
                                                                   SGGHDYDGVSYISNRPFFVLD--MSYLRNIT--VDMS-DDGGSAWVGAGATLGEVYYNIW
                                                                                                        SGGHCYED-----FVFDECVKAIINVTGLVESGYDDDRGYFVSSGDT-----NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TDVVYK------WQLVANKFPDNLFLRAMPQVV-----NGTKHGERTIAIVFWA
                                                                                                                                                                                                                                     poppy reticuline oxidase
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                  GB:AE005172; NID:g8570449;
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                                                                                                                                                                        25.4%;
                                                                                                                                                                                            10.8%;
                                                                                                                                                    73;
                                                                                                                                                                        Score 324.5; DB 2
Pred. No. 7.3e-17;
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                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                     PIDN: AAF76476.1;
                                                                                                                                                      169;
                                                                                                                                                                                            2;
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                                                                                                                                                      Indels
                                                                                                                                                                                         Length
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                                                                                                                                                      145;
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Maiti, R.; Marziali,
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404 362 344

462

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Tallon,

C. De Caralle Contraction of the Contraction of the

Qy 72 VRIVSGHCYEDEVFDECVKAIINVTGLVESGYD-DDRGYFVSSGDTNWGSFKTLF 126 113 LKIRSGHDYDGLSYISDRPF-FILDMSNIRDVSVDIASNGAWISAGATLGEVYYRIWEK 171  Qy 127 -RDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKY 185	1.; Me 1999 ATSP:F ne F21C 16; Len 116; I	Qy 393 PD-GLTSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVN 449	Db 165 QSSKTHGTHGFPAGVCPTVGAGGHISGGGYGNMIRKYGLSVDYVTDAKIV 214  Qy 179 EDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVI 228
Db 186 SQTLAFPAĞÜYÜPTÜĞAĞĞHİSĞĞĞFĞNLMÊKFĞITYDHVIDAQIIDVNGKLLN 238  Qy 188 KDSEGNDGELFWAHTGGGGGNEGIITKYYFKDLPMSPRQVIASNLHES 235	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-552 <sto> A;Cross-references: GB:AE005172; NID:g9797757; PIDN:AAF98575.1; GSPDB:GN00141 C;Genetics: A;Map position: 1 C;Superfamily: poppy reticuline oxidase Query Match Best Local Similarity 25.3%; Pred. No. 3.6e-15; Matches 128; Conservative 72; Mismatches 190; Indels 115; Gaps 24; Matches 128; Conservative 72; Mismatches 190; Indels 115; Gaps 24;  Oy 72 VRIVSGGHCYEDFVFDECVK-AIINVTGLVESGYDDDR-GYFVSSGDTNWGSFKTLFRDH 129 Db 127 LRIRSGGIDNEGGFSYMSSVPFVILDMHNLRSIDEVNLSKKNAWVQAGAT-LGELYVKINEA 185 OY 130 GRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDMLSGVEVVVFVLTEDSVLKYVH 187 OY 131 GRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDMLSGVEVVVFVLTEDSVLKYVH 187</sto>	RESULT 10  H86390  TIK7.21 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001 C;Accession: H86390 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: H86390	Qy  343DETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPD-GL 396  354 WDNRLNATQVDRKVFLDRNLDTSSFGKRKSDYVATAIPKKGIESLFKKMIELGKIGL 410  Qy  397 TSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQVGTYWQEEDKDAVNLKW 452

40,0

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A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: H84760
A,Status: preliminary
A;Molecule type: DNA
A,Residues: 1-532 <STO>
A,Cross-references: GB:AE002093; NID:g3033375; PIDN:AAC12819.1; GSPDB:GN00139
C,Genetics:
A,Gene: F1913.2; At2g34790
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-532 <ROU>
A;Residues: 1-532 <ROU>
A;Residues: 1-532 <ROU>
A;Experimental source: cultivar Columbia
A;Experimental source: cult
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A;Introns: 164/2; 326/3
C;Superfamily: poppy re
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Similarity 24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRIVSGGHCYEDFVF---DECVKAIINVTGLVESGYD-DDRGYFVSSGDT---NWGSFKT 124
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AGKSLFKNHFKAKSDFVKEPIPVEGLEGLWERFLE-----EDSPLTIWNPYGGMM
                                                                                                                                               ADIEQIYKTCEPTKALGGHAGWAPFP-VRPRKRHTSKTSYMHD--ETMDYPFYALTETI-
                                                                                                                                                                                                QDGTKVLYK-----WEQIADKLD-----DDLFIRVIISPASKTTKPGNRTISMSYQAQFL 318
                                                                                                                                                                                                                                            QDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSNDAE---REVAQDRHYHLE
                                                                                                                                                                                                                                                                                                                                             YVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFTRDAL 244
                                           -NGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQV-DMFGGEI 415
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; Pred. No. 4.9e-15;
88; Mismatches 197;
                                                                                                 FPELGLTKKDCTEMSWIKSVMYIAGFPNSAAPEALL 367
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A; Map position:
C; Superfamily: 1
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A;Residues: 1-532 <BEV>
A;Cross-references: EMBL:AL080254; GSPDB:GN00062; ATSP:F21C20.170
A;Experimental source: cultivar Columbia; BAC clone F21C20
C;Genetics:
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                                                                       ESGKGVFEGCYFNYPDVDL-----NNWKNGKYGALELYFLGNLNRLIKAKWLWDPNE 526
                                                                                                                           SEIADYETPFPHRKGNIYEIQYLNYWRGDVKEKY-MRWVERVYDDMSEFVAKSP-----
                                                                                                                                                                      HKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQV
                                                                                                                                                                                                                          RTRAS---LAFKAKSDFVQEPMPKTAISKLWRRLQE-----PEAEHAQLIFTPFGGKM
                                                                                                                                                                                                                                                                                                                           DDCTEMSWIESVIWFAE----LG----
                                                                                                                                                                                                                                                                                                                                                                       D-----IEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTE
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                         -RGAYINLRDLDLGMYVGVKRSKYEEGKSWGVK-YFKNNFERLVRVKTSVDPSD
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; pMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-527 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T1K7.22 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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Best Local Sim
Matches 138;
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                                                                                                                                                                                                                            363
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                                                                464
                                                                                                                                                                                                                                                                                                                                                                                             282 LFIRAWPQIVKGTKLG----ERTIG--VVF-----FAQFLGPT---DKLMEIMSQSLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 SVGLGGHIVGGGDGILARLHGLPVDWLSGVEVV-VKPVLTEDSVLKYVHKDSEGNDGELF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SVPFVILDMYNLRSITVDVSS-----KKAWVQAGAT-LGELYTKINEASQTLAFPAGVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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  __o
                                                              ---REALFNFRDFDIGINPSGLNVDEAKIYG--YKYFLGNLKRLMDVKAKCDPDNFFKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAHTGGGGGNFGIITKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVKAII-----NVTGLVESGYDDDRGYFVSSGDTNWGSFKTLFRDHGRVL--PGGSCY 139
                                                                                                                                                                               WDATAVAQRE-YIIKLQYQTYWQBEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQVESGK
                                                                                                                                                                                                                            STPGEFFKSKSDNIKKPIPKEGLEKIWK-----TMLKFNFVWIEFNPYGGVMDRIP
                                                                                                                                                                                                                                                                                                                                                    LEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETING 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVGVGGHITGGGFGNLMRKFGITVDHVIDAQLIGVNGKLLDRATM------GED--LF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVVYTPQGACTALD------RAMEKCSPGT---VRIVSGGHCYEDFVFDE
                                                                                                    GVFEGCYFNYPDVDLN-----NWKNGK-YGALELYFLGNLNRLIKAKWLWDPNEIFTNK 531
                                                                                                                                           ATATAFPHRKGNLFNLOYSTIWLDAKETENKLTMMKELY-EVAGPY
                                                                                                                                                                                                                                                                   SGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDALLQVDMFGGEIHKVV
                                                                                                                                                                                                                                                                                                              LGLRRED----CHEMSWFNTTLFWANYPVGTPTR-----VLLDRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    L-----LTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDRHYH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAIRGGGGASFGVILSWKINLVEVPKILTVFKVSKTLEQG--GTDVLYKWQLVATKVPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVSYTKNKRYSSLNYQKLVAIVAAKHVSHVQATVVCAKANGIQLRIRSGGHDYEGLSYTS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FÉCDEQSIP 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 298.5; DB 2;
Pred. No. 6.9e-15;
i8; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YFKDLPMSPRGVIASNLHFSWDGFTRDALQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 137;
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                                                                                                                                             463
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                     RESULT
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probable reticuline oxidase (EC
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1.5.3.9) -

opium poppy

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, 1 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: F86751
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C;Superfamily: poppy reticuline oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005172; NID:g4835780; PIDN:AAD30246.1; GSPDB:GN00141C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001 C;Accession: F86251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local &
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                                                                                                                                                                                                                                                                                                                                              344
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  501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 HKWQFVAPKTDPGLFMRLLLQPVTRNKMQTVRAS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SGGHCYED-----FVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWGSFKTLF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNTVMSMLTKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVL
                                                                                                                                                                    DFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDL--NNWKNGKYGALE----LYF
                                                                                                                                                                                                                                                                                   TSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVN--LKWIR 454
                                                                                                                                                                                                                                                                                                                                              VMWWANNDNATQIKPEILLDRNPDMATFGKRKSDFVEKEITKDGLDFLFKKMIEVGKIGL
                                                  LGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLKEPKQ 544
                                                                                                                 SFYSYM-APFVTKNPRHT---
                                                                                                                                                                                                                                                                                                                                                                                                 YMHDETMDYPFYALTETINGSGPNQR--GKYKSAYMIKDFPDFQIDVIWKYLTEVPD-GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVI----
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GENFDRLVKVKTAVDPQNFFRDEQSIPTLPGKPARR 536
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                                                                                                                                                                                                                             --FNPYGGIMSTVATTKTPFPHRKKLYKIQHSMNWKDPGTEAETSFLQKAK
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24.2%; Pred. No. 1.1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Mismatches 190;
                                                                                                                 ----YINYRDLDIGVNTPGPNSYRVAEVFGRMYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FPELGLKKENCTEMTWIQS
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C;Accession: T07969
R;Facchini, P.J.; Penzes, C.; Johnson, A.G.; Bull, D.
Plant Physiol. 112, 1669-1677, 1996
A;Title: Molecular characterization of berberine bridge enzyme genes from opium A;Reference number: Z16255; MUID:97127853; PMID:8972604
A;Accession: T07969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Roses: 1-535 <FAC>
A;Cross-references: EMBL:AF025430; NID:g3282516; PIDN:AAC61839.1; PID:g3282517
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: berberine bridge enzyme
C;Species: Papaver sommiferum (opium poppy)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 15-Jun-2001
C;Accession: T07969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: bbel
C;Superfamily: poppy reticuline oxidase
C;Keywords: oxidoreductase
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485
                                                                                                        438
                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                          399 AEMKDALLQVDMFGGEIHKVVWDATAVAQR-----EYIIKLQYQTYWQEEDKDAVN-- 449
                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                                   342 HDETMDYPFYALTETINGSGPNORGKY-KSAYMIK-DFPDFQIDV-IWKYLTEVPDGLTS 398
                                                                                                                                                                                                                                                                                                                                                                                                                             305 RKDAAKTIIDEKFPELGLVDKEFQEM------SWG-----SWG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 -NDAEREVAQDRHYHL---EADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYM 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 IEDASSLLHKWQ-YVADELDEDFT-----VSVLGGV----NGNDAWLMFLGLHLG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 LI-DSNGAILDREKMGDD--VFWAIRGGGGGVWGAIYAWKIKLLPVPEKLTVFRVTKNVG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 LTEDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 TDTLGF-----TAGWCPTVGSGGHISGGGFGMMSRKYGLAAD-----NVVDAI 202
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                                                 506 L----YFLGNLNRLIKAKWLWDPNEIFTNKQSIP 535
                                                                                                                                                       450 LKWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLN--NWKN--GKYGALE 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 ---ASNLHFSWDGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TNWGSFKTLFRDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVBVVVKPV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TVRIVSGGHCYE------DFVFDECVKA-----IINVTGLVESGYDDDRGYFVSSGD 116
IARNWGERYFSSNYERLVKAKTLIDPNNVFNHPOSIP 521
                                                                                                      SEWLAKFYDYL-----EPFVSKEPRVG-----YVNHIDLDIGGIDWRNKSSTINAVE
                                                                                                                                                                                                              SEOPGGFIALNGFGGKMSEISTDFTPFPHRKGTKLMFEYIIA-----WNQDEESKIGEF 437
                                                                                                                                                                                                                                                                                                                    --ESM--AFLSGLDTISELN-NRFLKFDERAFKTKVDFTKVSVPLNVFRHALEM----L 383
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                                                                                                        184
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Search completed: June 10, 2003, 10:00:28 Job time : 25 secs

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Minimum DB
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Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution. being printed, to have a

## SUMMARIES

Result No.		Query Match Length DB	Length	DB	ID	Description
ב ו	2997	100.0	546	22	AAU02192	Synthetic hexose o
Ŋ	2997	100.0	546	22	AAB59205	Chondrus cripus he
w	2989	99.7	546	18	AAW20076	Hexose oxidase, an
4	2985	99.6	546	21	. AAY83619	Synthetic hexose o
ຫ	635.5	21.2	539	20	AAY39306	SpnJ protein invol
6	635.5	21.2	539	22	AAB70952	<ol><li>S. spinosa protein</li></ol>
7	368.5	12.3	530	23	ABB91135	Herbicidally activ
ω	347.5	11.6	539	23	ABB93022	Herbicidally activ
9	333.5	11.1	529	23	ABB91138	Herbicidally activ
10	328.5	11.0	535	23	ABB91134	Herbicidally activ

<b>4</b> 5	44	43	42	41	40	9 9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
240	240	240	249.5	249.5	249.5	252	255	263	264.5	265.5	266	272	272.5	272.5	274	275	277	277	277	277.5	278	286.5	290.5	292.5	294.5	294.5	294.5	296	298.5	$\circ$		306.5		324.5
8.0	8.0	8.0	8.3	8. <sub>3</sub>	8.3	8.4	8.5	8.8	8.8	8.9	8.9	9.1	9.1	9.1	9.1	9.2	9.2	9.2	9.2	9.3	9.3	9.6	9.7	9.8	•	9.8	•	•	•	•	•	10.2	10.7	10.8
534	527	527	551	540	474	531	495	508	421	544	540	529	530	525	529	529	529	527	508	526	533	538	535	509	556	541	458	536	527	532	552	545	540	541
21	23	21	21	21	21	23	20	19	21	22	19	19	21	21	22	19	22	23	19	23	23	22	22	19	21	21	21	23	23	23	23	21	23	23
AAG42978	ABB91196	AAG42979	AAG29443	AAG29444	AAG29445	ABB91195	AAY24919	AAW55060	AAG43379	AAB81081	AAW55059	AAW55054	AAG43377	AAG43378	AAB61788	AAW55053	AAB61787	ABB91194	AAW55061	ABB91197	ABB91198	AAB61790	AAB61789	AAW55062	AAG41843	AAG41844	AAG41845	ABB90968	13	ABB93020	ABB91137	839	ABB93021	ABB90805
Arabidopsis thalia		₼	S	Arabidopsis thalia		~	Microdochium nival	O1		μ.	Lettuce antifungal	Sunflower leaf ant	Arabidopsis thalia	Arabidopsis thalia	Sunflower carbohyd	н	carb	_	Arabidopsis antifu	Herbicidally activ	~	California poppy r	Opium poppy reticu				Arabidopsis thalia	Herbicidally activ				3	Herbicidally activ	Herbicidally activ

## ALIGNMENTS

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Synthetic hexose oxidase (HOX) amino acid sequence.
                                    12-SEP-2001
                                                                         AAU02192;
                                                                                                            AAU02192 standard; Protein; 546
                                    (first entry)
                                                                                                              Ä
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HOX; seaweed; hexose oxidase; interleukin I receptor antagonist; IL-1ra; food manufacturing; beverage; detergent; baking; dough improving agent; D-hexose:02-oxireductase; EC 1.1.3.5.

Chondrus crispus.

ARUSULT 1
AAUU2192
ID AAUU2
XX AAUU2
XX AAUU2
XX AAUU2
XX Synt
XX Synt
XX HOX,
KW HOX,
KW D-ha
XX Chorr
OS Synt
XX WO20
XX W10XX Synt
XX W10XX W21
XX W21
XX W21
XX W21
XX W31XX W41
XX Jaha
XX UAN
XX 24-NOV-2000; 2000WO-IB01886. 31-MAY-2001. WO200138544-A1 Synthetic. 24-NOV-1999; 99GB-0027801.

WPI; 2001-367695/38. N-PSDB; AAS06173. Johansen CL, Zargahi MR; (DANI-) DANISCO AS. Kjaerulff S, Madrid SM, Pedersen H, Poulsen CH;

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CC a soluble or membrane associated intracellular protein of interest (POI)
CC from a cell involving contacting a cell comprising a soluble or membrane
CC associated intracellular POI with a membrane extracting composition (I)
CC and causing the POI to be released from the cell in a soluble form. The
CC method is useful for releasing POI, such as an interleukin I receptor
CC antagonist (IL-1ra) which involves contacting a transformed cell
CC comprising IL-1ra with (I) and causing IL-1ra to be released from the
CC transformed cell, in a soluble form. The method is also useful for
CC screening mutated cells or transformed cells producing elevated levels of
CC intracellular POI. The method is used to release a POI for manufacturing
CC food products, such as beverages, preparation of detergents, and in
CC baking as a dough improving agent. The method obtains a fast, specific
CC and economically efficient extraction of a soluble or membrane associated
CC intracellular POI without the use of conventional cell disruption
CC techniques. The resulting cell extract contains less contaminating
CC intracellular POI can be recovered from a eukaryotic host organism such
CC as yeast, before glycosylation takes place. The method can be used to
CC meadium.
CC meadium.
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Best Local S
Matches 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                    RDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEBFVMYLYTSYSNDABREVAQDRHYHL
EADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETINGS
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Pred. No. 3.9e-281;
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DATAVAGREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQVESGKGV

480

420 420

DATAVAQREYIIKLQYQTYWQBBDKDAVNLKWIRDFYBEMYBPYGGVPDPNTQVESGKGV FEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK 540

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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                  The present invention relates to a new anti-fouling composition. The composition involves a surface coating material, a hexose oxidase enzyme obtained from a marine organism and a substrate for the enzyme. The anti-fouling composition is useful as a coating formulate for treating a surface, e.g. outdoor wood work, external surface of a central heating system, or a hull of a marine vessel. It is also useful as an anti-fouling agent for marine structures exposed to seawater flora and fauna.
                                                                                                                                                                                                                                                                                                                                                                                                                            New anti-fouling composition, useful as a coating for different surfaces, e.g. outdoor woodwork, external central heating system, or a hull of a marine vessel
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 35-36; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-2000; 2000WO-IB00829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexose oxidase; marine alga; anti-fouling
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                     SVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVIASNLHFSWDGFT
                                                                 SFKTLFRDHGRVLFGGSCYSVGLGGHIVGGGDGILARLHGLFVDWLSGVEVVVKFVLTED 180
                                                                                                                          DRAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYFVSSGDTNWG 120
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Pred. No. 3.9e-281;
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AAW20076 shows the hexose oxidase (HO) enzyme of the marine algae species Chondrus crispus. HO is useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can be recombinantly produced in industrially appropriate quantities, and at a quality and purity level which renders the polypeptide suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hexose oxidase; Chondrus crispus; marine algae; recombinant; antimicrobial; antioxidant; food preparation; dairy product; starch; beverage; animal feed; silage; sugar reduction; cosmetics; dental; toothpaste; dough; lactone production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW200976 standard; Broteing SAG A
                                                                                                                                                                                                                                       Recombinant production of polypeptide having hexose oxidase activity - used in food preparations as antibacterial and antioxidant agent
                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chondrus crispus.
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                                                                                                                                                                                                                                                                                                                                          Hansen OC,
                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                        Example 3.5; Page 95-97; 124pp; English.
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                                                                                                                                                                                     Synthetic hexose oxidase.
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                                               01-DEC-1999;
                                                                                                 EP1008651-A2
                                                                                                                        Synthetic
                                                                                                                                               prokaryote;
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                       09-DEC-1998;
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                                                                                                                                                            Hexose oxidase; production;
 (BIOT-) BIOTEKNOLOGISK INST
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                                                 99EP-0204068
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Pred. No. 2.4e-280;
0; Mismatches 1;
                                                                                                                                                            fermentation; synthetic; modification;
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                                          EPKOTK 546
                                                                                                                                                                                                                                                                                                                                                                                        EADIEQIYKTCEPTKALGGHAGWAPFPVRPKRHTSKTSYMHDETMDYPFYALTETINGS
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                                                                                                                                                                                                         DATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQVESGKGV
                                                                                                                                                                                                                                                                      GPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTTAEMKDALLQLDMFGGEIHKVVW
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EPKOTK
                                                                                                               FEGCYFNYPDVDLNNWKNGKYGALELYFLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK
                                                                                                                                                                               DATAVAQREYIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQVESGKGV
                                                                                                                                                                                                                                                                                                                                                                EADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDETMDYPFYALTETINGS
                                                                                       FEGCYFNYPDVDLNNWKNAKYGALELYFLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSNDAEREVAQDRHYHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pedersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2985; DB 21;
Pred. No. 5.7e~280;
2; Mismatches 1;
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RESULT

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Query Match Best Local S Matches 174

Similarity

21.2%; Score 635.5; DB 20 30.2%; Pred. No. 2.5e-52; tive 91; Mismatches 216;

DB 20;

Length 539;

Gaps

16;

B

Conservative

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This is the amino acid sequence of the product of the spnJ gene. The CC protein is involved in spinosyn biosynthesis. The SpnJ gene is one of 23 CC genes and open reading frames contained in an 80kb DNA sequence CC ARZAISO1. Spinosyns are insecticidal microlides which are useful for the CC control of arachnids, nematodes and insects. Biosynthesis of spinosyns CC cours via stepwise condensation and modification of carboxylic acid CC precursors generating a linear polyketide which is modified further. The CC DNA sequence contains a central region of approximately 55kb which has CC homology to the DNA encoding the polyketide synthases (PKS) of known CC macrolide producers. The spinosyn PKS DNA region consists of 5 ORFs with CC stop codons at the end of acyl carrier protein (ACP) domains. Together the PKS polypeptides (AAY3929-Y39301), form a complex consisting of an CC initiator module, spnA, and several extender modules spnB-spnE. The CC products of the genes present in the region upstream of the PKS genes are spinosyn biosynthesis. There are also two CRFs ORFILS and ORFIL6 present immediately upstream of the PKS genes CC nownstream of the PKS region producing polypeptides AAY39316-Y39317, and two ORFS ORF1 and ORF2 present CC downstream of the PKS region producing polypeptides AAY39318-Y39319. It is suggested that SpnJ is involved in oxido reduction during spinosyn complex consistion of spinosyns, and consynthesis. The genes are useful to improve yields of spinosyns, and cfor creating new spinosyns e.g. by mutagenesis, or interruption of steps of spinosyn biosynthesis. The modified spinosyns may be a new insect control agent or serve as substrates for further chemical modification cuseful to isolate similar sequences from S. spinosa or other species by Chybrides and control spinosyns are also useful to isolate similar sequences from S. spinosa or other species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase; insecticide; oxido-reduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 153-154; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spinosyn biosynthetic genes from Sau
for production of insecticidal spinosyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-1999;
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J, Turner JR,
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                                        WPI; 200;
N-PSDB;
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New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
                                                                                                        Eberz G,
                                                                                                                                                                                       27-AUG-1999;
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DB; AAF88322.
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhammose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express or derivatives, including production of transgenic plants that express or derivatives for sequencing of the Saccharopolyspora spinosa genome. (II) are markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying capression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents an S. spinosa C-C cyclising enzyme.
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Best Local Similarity 30.3
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 RAMEKCSPGTVRIVSGGHCYEDFVFDECVKAIINVTGLVESGYDDDRGYF-VSSGDTNWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 DAVR--TGRRVGVRSGGHCFENLVADPAIRVLVDLSELNRVYYDSTRGAFAIEAGAALGO 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 APMNRTPGTEI-----TVEPDDPRYPDLVVGHNPRFTG-KPERIHIASSAEDVVHAVA
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                                                     LGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLKEPKQ 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYRTLEKNWGVTIPTGACPGVGAGGHILGGGYGPLSRREGSVVDYLQGVEVVVVDQAGEV
                                                                                                                                                                                             KWIRDFYEEMYEPYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNN--WKNGKYGALELYF 508
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                                                                                                                                           TWIRGFYREMYAETGGVPVPGTRV---
                                                                                                                                                                                                                                                                                                                                             EVPDGLTSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVNL
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KDNYPRLQRAKARWDPQNIFQHGLSIKPPARLSPGQ 538
                                                                                                                                                                                                                                                                            ----VYGYDNPAAALLLLGYGGMANAVAPSATALAQRDSVLKALFVTNWSEPAEDERHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPVRP 330
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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VDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGG
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                                                                                                                                                                                                          TDALMAIMNONWPELGLK--HEDCOEMSWLNSTLFWADYPA-----GTPTSIL----LD
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                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 349; 261pp + Sequence Listing; English.
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Best Local S
Matches 128
           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                 Tietjen K,
                                                                                                                                28-AUG-2001; 2001WO-EP09892
                                                                                                                                                        28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                               07-FEB-2002
                                                                                                                                                                                                       WO200210210-A2
                                                                                                                                                                                                                              Arabidopsis
                                                                                                                                                                                                                                                    Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                          Herbicidally active polypeptide
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                                                                                                          BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                     WLWDPNEIFTNKQSIP 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFRDHGRVL--PGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKILNRASMGED--LFWAIRGGGGASFGVILSWKI-NLVKVPKILTVFKVNKTLEQGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPR--GVIASNLHFSWDGFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINEASQTLAFPAGVCPTVGVGGHISGGGYGNLMRKFGITVDHVSDAQLI------DVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGKYGALEL-----YFLGNLNRLIKAK 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFNPYGGVMDQIPSTATAFPHRKGNMFKVQYSTTWLAANATEISLSMMKELY-KVAEPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVDMFGGEIHKVVMDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYBPYG
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25.8%;
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Pred. No. 4.4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
07-FEB-2002
                                                       Arabidopsis thaliana
                                                                                    Herbicidal;
                                                                                                                Herbicidally active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                              WO200210210-A2
                                                                                                                                             31-MAY-2002
                                                                                                                                                                         ABB90805
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                                                                                                                                                                                                                                                                                                                                                                                             VWLHFNPYGGMMDRIPSNATAFPHRKGNLFKVQYYTTWLDPNATESNLSIMKELY-EVAE
                                                                                                                                                                                                                                                                                                                                                                                                                      L-LQVDMFGGEIHKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRIVSGGHCYEDFVFDECVKAII------NVTGLVESGYDDDRGYFVSSGDTNWGSFKT
                                                                                                                                                                                                                                                                                                       LIKAKWLWDPNEIFTNKQSIP 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPDGLTSAEMKDA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --QDRHYHLEADIEQIY-----KTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMHDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDALQDLLTKYFKLARCDWKNTVGKF--QIFHQAAEEFVMYLYTSYSNDAEREVA----
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                                                                                                                                                                                                                                                                           LMDVKAKSDPENFFKNEQSIP 523
                                                                                                                                                                                                                                                                                                                                                               PYGGVPDPNTQVESGKGVFEGCYFNYPDVDLNNWKNGK-----
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ilarity 27.5%;
Conservative 6
                                                                                    plant; agriculture;
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                                                                                                               polypeptide
                                                                                                                                           entry.
                                                                                                                                                                                                                                                                                                                                    VSSNP---REAFFNYRDIDIGSNPSGETDVDEAKIYG--YKYFLGNLKR
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                                                                                                                                                                                                    541
                                                                                     herbicide
                                                                                                                SEQ ID
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target comprising aligning and c from plant with nucleic a
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501 G--RKYFGENFDRLVKVKTAVDPENFFRDEQSIPTLPTK
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                        GALELYFLGNLNRLIKAKWLWDPNEIFTNKQSIPTKPLK
                                                                                                               GKLGLV--
                                                                                                                                                                                               RHTSKTSYMHDETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEV
                                                                                                                                                                                                                                                     LYTSYSNDAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWA----PFPVRPR---K
                                                                                                                                                                                                                                                                                                                ASNLHFSW-----
                                                                                                                                                                                                                                                                                                                                                                      EDSVLKYVHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVI------
                                                                                                                                                                                                                                                                                                                                                                                               QSSKT----HGTHGFPAGVCPTVGAGGHISGGGYGNMIRKYGLSVDYVTDAKIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGHDYDGVSYISNRPFFVLD--MSYLRNIT--VDMS-DDGGSAWVGAGATLGEVYYNIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGHCYED-----FVFDECVKAIINVTGLVESGYDDDRGYFVSSGDT-----NW 119
                                                       MEKTRSFYSYM-APFVTKNPRHT
                                                                                LKWIRDFYEEMYEFYGGVFDFNTQVESGKGVFEGCYFNYFDVDL-----
                                                                                                                                        PD-GLTSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEEDKDAVN--
                                                                                                                                                                    RNPDSASFL-
                                                                                                                                                                                                                            LFLGKQSDLMSLLTKE---FPELGLKP--ENCTEMTWIQSVMWWANNDNATVIKPEILLD
                                                                                                                                                                                                                                                                                    ALDMVHKWQFVAPKTSPDLFMRLMLQPVT-----RNTT-----
                                                                                                                                                                                                                                                                                                                                          -DVNGRILDRKSMGED--LFWAIGGGGGASFGVILSFKIKLVPVPPRVTVFRVEKTLVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541
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25.4%; Pred.
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                                                                                                              - FNPYGGKMSEVATTATPFPHRKRLFKVOHSMNWKDPGTDVESSF
                                                                                                                                                                                                                                                                                                              DGFTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324.5;
No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      b; DB
                                                      --YLNYRDLDIGINSHGPNSYREAEVY
                                                                                                                                                                      KRKSDYVEKEISKDGLDFLCKKLMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 145;
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                                                                                  NNWKNGK-Y
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Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 2232; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as
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354
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                                                                                                                                                                                                                                                                                                                                                                                                                     186 VHKDSEGNDGELFWAHTGGGGGNFGIITKYYFKDLPMSPRGVI------ASNLHFS 235
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                                                        ----DETMDYPFYALTETINGSGPNQRGKYKSAYMIKDFPDFQIDVIWKYLTEVPD-GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRVHG--FPAGVCPTVGVGGHLSGGGYGNMVRKFGLSVDYVEDAKIV-----DVNGRV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRIVSGGHCYE--DFVFDECVKAIINVTGLVESGYD-DDRGYFVSSGDTNWGSFKTLF--
WDNRLNATQVDPKVFLDRNLDTS---SFGKRKSDYVATAIPKKGIESLFKKMIELGKIGL
                                                                                                                                                                                                                                                                                                                     WDG----
                                                                                                                                                                                                                                                                                                                                                                          LDRKAMGED--LFWAITGGGGGSYGVVLGYKVKLVPVPSVVTVFRVEQYMDSGAVDMVHK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RDHGRVLPGGSCYSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKIRSGGHDYDGLSYISDKPF-FILDMSNIRDVSVDIASNSAWISAGATLGEVYYRIWEK 171
                                                                                                                                                                                     DAEREVAQDRHYHLEADIEQIYKTCEPTKALGGHAGWAPFPVRPRKRHTSKTSYMH----
                                                                                                                                                                                                                                                   WQSVGPKTDPNLFMRMLIQPVTRKKVKTVR-----ASVVALFLGRADEVVALLSKEF--
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                                                                                                                                                                                                                                                                                                               FTRDALQDLLTKYFKLARCDWKNTVGKFQIFHQAAEEFVMYLYTSYSN 286
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RESULT 13
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                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 139;
                                                                                                                                                                                                                                                                                                                                         This sequence represents the Cannabis sativa tetrahydrocannabinolic acid (THCA) synthase amino acid sequence. The THCA gene sequence can be used to produce an expression vector containing the gene. Cells can be transformed using the vector, so that they produce a protein with THCA synthase activity. THCA can be used for anaesthesia, pain-killing, intraocular pressure lowering and anti-inflammatory treatment.
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahydrocannabinolic acid synthase; THCA; anaesthesia; paintraocular pressure lowering; anti-inflammatory treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetrahydrocannabinolic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 8-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tetrahydrocannabinolic acid synthase
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228
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                                                                                           YSVGLGGHIVGGGDGILARLHGLPVDWLSGVEVVVKPVLTEDSVLKYVHKDSEGNDGELF 198
                                                                                                                                                                                      NLRFISDTTPKPLVIVTPSN--NSHIQATILCSKKVGLQIRTRSGGHDAEGMSYISQVPF
                                                                                                                                                                                                                   NRRWIGTNIDFVYVVYTPQGACTALDRAMEKCSPGT---VRIVSGGHCYEDFVFDECVKA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSAEMKDALLQVDMFGGEIHKVVWDATAVAQREYIIKLQYQTYWQEE----DKDAVNLKW 452
WAIRGGGGENFGIIAAWKIKLVAVPSKSTIFSVKKNMEIHGLVKLFNKWQNIAYKYDKDL
                             WAHTGGGGGNFGIITKYYFKDLPMSPRGVIAS-----NLHFSWDGFTRDALQDL
                                                            PTVGVGGHFSGGGYGALMRNYGLAAD-----NIIDAHLVNVDG--KVLDRKSMGED--LF
                                                                                                                         VVVDLRNMHSIKIDVHSQTAWVEAGATLGEVYY-----WINEK----NENLSFPGGYC
                                                                                                                                                          II-----
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                                                                                     The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDGFTRDALQDLLTKYFKLARCDWKNTV-----GKFQIFHQAAEEFVMYLYTSYSNDAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAAMGED--LFWA-IRGGGSSFGVILSWKINLVEVPKILTVFKVNKTLEQG--GTDILYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                              516 FFCDEQSIP 524
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                                                                                                                                                                                                                                                                             416 HKVVWDATAVAQRE-YIIKLQYQTYWQEEDKDAVNLKWIRDFYEEMYEPYGGVPDPNTQV 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 PTVGVGGHFSGGGYGTLLRKHGLAADHVIDARVV------DARGRILERREMGED--FF
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                                                                                                                                                        ESGKGVFEGCYFNYPDVDL------NNWKNGKYGALELYFLGNLNRLIKAKWLWDPNE 526
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                                                                                                                                                                                                                                                                                                                         RTRAS---LAFKAKSDFVQEPMPKTAISKLWRRLQE----PEAEHAQLIFTPFGGKM
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